Segment - User Manual

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Software platform v2.0 R4790

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1 Regulatory status

Segment may be used for either investigational off label use or commercial purposes. Please see license terms which license form that apply to you. Users are also required to investigate the regulatory requirements pertinent to their country or location prior to using Segment. It is in the users responsibility to obey these statues, rules and regulations.

1.1 Commercial usage of Segment

FDA approved versions of Segment are identified with a labelling upon start up displaying licence details and the FDA 510(k) number K090833. If your version does not display this information your version is not FDA approved and you need to contact Medviso AB to receive a such license.

Please note that there are features that are not included in the FDA approval. These functions are marked in this User Manual that they are only for investigational use.

1.2 Indications for use

Segment is a software that analyzes DICOM-compliant cardiovascular images acquired from magnetic resonance (MR) scanners. Segment specifically analyzes the function of the heart and its major vessels using multi-slice, multi-frame and velocity encoded MR images. It provides clinically relevant and reproducible data for supporting the evaluation of the function of the chambers of the heart such as left and right ventricular volumes, ejection fractions, stroke volumes, peak ejection and filling rates, myocardial mass, regional wall thickness, fractional thickening and wall motion. It also provides quantitative data on blood flow and velocity in the arterial vessels and at the heart valves. Segment is tested on MR images acquired from both 1.5 T and 3.0 T MR scanners. The data produced by Segment is intended to be used to support qualified cardiologist, radiologist or other licensed professional healthcare practitioners for clinical decision making. **It is a support tool that provides relevant clinical data as a resource to the clin-**

ician and is not intended to be a source of medical advice or to determine or recommend a course of action or treatment for a patient.

1.3 Investigational purposes

None of the organizations/persons named in conjunction with the software can accept any product or other liability in connection with the use of this software for investigational purposes.

2 License Terms

The software can be used under three different license forms. More detailed information and pricing of the different license forms is given on Medviso AB homepage `http://www.medviso.com`.

2.1 Free or charge for non-commercial research

The software is free to use for non-commercial research or educational purposes if and only if you reference it properly and send full bibliographic information (such as Pubmed link) of your final work when published or accepted for publication. Details on how to reference the software are given in Chapter 40.

You may not use the software for clinical routine or commercial applications such as company paid pharmaceutical trials without contacting the author. Details about commercial/clinical use is given below. Note that the software is copyright and may not be redistributed/resold without permission of the author.

2.2 Commercial or Clinical use

To use the software for clinical routine or commercial research (see above) you need a commercial license of Segment. Details on how to acquire a such license are found on the homepage `http://www.medviso.com`. This version of Segment is FDA 510(k) approved, K090833. The license includes some extended functionality in forms of different modules that are not available in the free research only version. Depeding on the exact configuration your commercial version may include some or all of the following extra features.

- Support! Details about the support is given in Chapter 41.
- Report sheet generator. In this module it is possible to print a report sheet with a results and free text annotations as a patient report. This is described in Chapter 38.

- Native Bruker file format reader. The Native Bruker file format support module allows you to directly load Bruker files into Segment. This is described in Chapter 37.
- Segment patient database. This allow you to easily find and load your patient images. This module is further described in Segment Database User Manual.
- Segment DICOM server module. This module allows Segment to work as a standalone workstation and receive images directly from the scanner, a hospital PACS, or another DICOM workstation. This module is further described in Segment Database User Manual.
- Segment PACS connection module. This module allows you to download and export images directly to a PACS system. This module is further described in Segment Database User Manual.
- Sectra Plug-in Module. This will allow you to run Segment as a plug-in to Sectra PACS.

2.3 Commercial research (non-human images)

There is also a non FDA approved version for commercial purposes of Segment available. This license type is intended for commercial R & D companies, or industry sponsored trials where the majority (more than 50%) of the funding comes from a commercial sponsor.

2.4 Future modules

Then there are also a few modules that are not yet available to the research community, but will be made freely available when we have published methods paper describing the adequately.

- Strain analysis from velocity encoded MRI images.
- T2* Module.
- Automated whole heart segmentation of CT images.
- Automated bone segmentation of CT images.
- Volume Rendering Module.
- ...

3 Acknowledgements

Even if this project started as a one man project, it has grown and it would never been possible without the help of many many people.

Financial support has been received from the Swedish Heart-Lung foundation, Swedish Research Council, local founds from Östergötland County, and Region of Scania.

I would like to acknowledge all the people that have put in feed back on usability and desired functionality, algorithm etc. Among others: Andreas Otto, Andreas Sigfridsson, Erik Bergvall, Erik Hedström, Henrik Haraldsson, Henrik Engblom, Håkan Arheden, Jan Engvall, Lars Wigström, Lisa Hård af Segerstad, Karin Markenroth Bloch, Marcus Carlsson, Martin Ugander, Mikael Kanski. Finally thank to you all Segment users in the research community that has inspired and contributed to the development.

Special thanks to code providers Erik Bergvall (core routines of strain analysis), Helen Soneson (strain analysis module, SPECT module, Image fusion module), Shruti Agarwal (refactory of strain analysis module), Jonatan Wulcan (Sectra Plugin module and general improvements), Johannes Töger (3D flow and volume tracking), Mårten Larsson (3D flow and kinetic energy).

Commercial development has been done by Jane Sjögren (improvements to general object segmentation, implementation of prototype based segmentation, CT functionality, and graphical seriesselector). General debugging and implementation of the new interpolated contours has been done by Johan Ugander and Erik Södervall. Report Module and general debugging have been performed by Nils Lundahl.

4 Rationale for the Software

Developing this software have required a lot of work. So what has the rationale been for producing new software where there are commercially available software packages that at least partially could do the same thing?

- At the time of writing the core of the program other existing software were simply not good enough.
- Existing software packages did not allow to store the segmentation and regions of interest in a flexible way.
- Existing software packages had no flexible exporting capabilities to allow full usage of automated delineation algorithms.
- A freely available software greatly facilitates and improves possibilities to do multi-center studies.
- There will be no company secrets we will always know, and be open and tell you exactly how things are implemented. This is crucial for doing good research.
- It can serve as a platform for experimenting and testing of various image processing ideas.
- It has been given very valuable experience of how to handle and develop a large scientific software package.

As the software grew in capabilities, there also started to be a commercial interest in the software. However, Segment will always be tightly coupled to cardiovascular research and continue to be freely available for research purposes. We hope that you will find the software useful in your research, and please do not hesitate to tell us what you think about it, and come with suggestions for improvements.

The software has been developed at:

- Home during late evenings and weekends.
- Linkï¿½ping University, Sweden, Centre of Medical Image Science and Visualization & Department of Medicine and Care, Clinical Physiology (2002-2004).

- Cardiac MR Group, Lund University, Department of Clinical Physiology (2005-present).
- The company Medviso AB (2007-present).

5 How to Read This Manual

Technical documentation always face a certain dilemma: whether write for top-down or bottom-up learners. A top-down learner prefers to read or skim documentation, getting a large overview of how the system works; only then does she actually start using the software. A bottom-learner is a 'learn by doing' person, someone who just wants to dive into the software and figure it out as she goes, referring to book sections when necessary.

This documentation is biased towards top-down learners (And if you're actually reading this section, you're probably already a top-down learner yourself!) However, if you're a bottom-up person, don't despair. If you have patience enough to ready only one chapter then read Chapter 10. If you then get stuck you may use this manual to search for specific solutions. Most of the icons and pushbuttons in the software have tooltip strings attached to them. Simply point the mouse over a button and you will have feeling on what purpose it has.

If you do not want to read the manual at all, you can instead see the on-line video tutorials. They are available under the Help menu.

6 Conventions and Abbreviations

This chapter describes the typographic conventions and used abbreviations in this manual and in the program.

6.1 Typographic conventions

`A`	Key `A` at the keyboard.
`Ctrl-A`	Control key. Hold down `Ctrl` key and `A` simultaneously.
	Icon in toolbar.
`*.mat`	Filename extension.
`C:/Program`	Folder.
File	Menu, e.g. File menu.
File→Save As	Sub menu, e.g. under the File menu the item Save As is found.
Close	Push/Toggle button in the graphical user interface.
◎ Endocardium	Radiobutton in the graphical user interface.
☒ Single frame	Checkbox in the graphical user interface.

6.2 Trademarks

Below are some of the trademarks used in this manual.

- Segment is a trademark of Medviso AB.
- Segment DICOM Server is a trademark of Medviso AB.
- Sectra PACS is a trademark of Sectra Imtec AB, (`http://www.sectra.se`).
- Matlab is a trademark of the Mathworks Inc, (`http://www.mathworks.com`).

6.3 Abbreviations

2CH	Two chamber view
3CH	Three chamber view
4CH	Four chamber view
3D	Three Dimensional

3D+T	Time Resolved Three Dimensional
AA	Ascending Aorta
ASW	Anterior Septal Wall Thickness
ARD	Aortic Root Diameter
BPM	Beats per minute
BSA	Body Surface Area
CMR	Cardiac Magnetic Resonance
CO	Cardiac Output
CT	Computed Tomography
DA	Descending Aorta
DE-MRI	Delayed Enhancement MRI
ED	End diastole
EDD	End Diastolic Dimension
EDL	End Diastolic Length
EDV	End Diastolic Volume
EF	Ejection Fraction
ES	End systole
ESD	End Systolic Dimension
ESL	End Systolic Length
ESV	End Systolic Volume
FWHM	Full Width Half Maximum
GUI	Graphical User Interface
HR	Heart Rate
LV	Left Ventricle
LVM	Left Ventricle Mass
MaR	Myocardium at Risk
MO	Microvascular obstruction
MB	Mega Byte
MIP	Maximum Intensity Projection
MPR	Multiplanar Reconstruction
MR	Magnetic Resonance
MRI	Magnetic Resonance Imaging
PET	Photon Emission Tomography
PER	Peak Ejection Rate
PDW	Proton Density Weighted
PFR	Peak Filling Rate
PLW	Posterior Lateral Wall Thickness
PWV	Pulse Wave Velocity

ROI	Region Of Interest
RV	Right Ventricle
RVmaj	Right Ventricle Major Axis
RVmin	Right Ventricle Minor Axis
SPECT	Single Photon Emission Computed Tomography
SSFP	Steady State Free Precision
SV	Stroke volume
TOF	Time of Flight
VENC	Velocity Encoding limit

7 System Requirements

In this chapter the hardware requirements for the software are outlined. Possible bottlenecks are (in order of likelihood) lack of RAM memory, CPU speed, and I/O network or disk transfer rates.

7.1 Operating system

Segment is available both as a precompiled application and also a source code version. Precompiled versions are available for the following platforms:

- Microsoft Windows. It will run on any of the following Windows 2000, Windows XP (32 bit), Windows XP (64 bit), Windows Vista (32 bit), Windows 7 (32 bit), Windows 7 (64 bit), Windows 8.
- The Segment have been reported to run well on Mac using Parallels.

The source code version is available for the following platforms:

- Windows 32
- Windows 64
- Linux 64

To run the source code format you need Matlab R2011a or later.

7.2 Hardware requirements

The list below are the recommended hardware requirements. To run a clinical versin of Segment you need at least the specifications indicated below.

- A fairly recent computer with 4 GB of memory or more.
- Harddisk with at least 500 MB of available space. The program Matlab Compiler Runtime takes about 450 MB, another 20MB is taken by the program.
- Graphics card supporting both DirectX and OpenGL (hardware accelerated) is recommended. Systems with two screens is recommended for clinical usage of Segment.

We strongly recommend using SSD disk for reading data.

8 Installing and Uninstalling

The descriptions for first time installation is divided into two main sections, describing Windows standalone installation (section 8.1) and source code installation (section 8.2), respectively. The sections after that describes general settings that should be performed regardless of installation type.

8.1 Installation of Standalone version for Windows

This section is written for first time installation of Segment. For upgrading, see the Section 8.4. The program is written in Matlab, in order to run it you therefore need to install Matlab Compiler Runtime first. **Note** that to be able to perform these steps below you **need** to have administrator privileges on the machine. If you are using Windows Vista, then please also refer to Section 8.1.4.

8.1.1 Installing Matlab Compiler Runtime

If you have Matlab **and** Matlab Compiler Runtime (MCR) installed on your computer this step may not be necessary, provided that you have exactly the same version as used for compiling Segment. Currently Matlab Compiler Runtime R2014a is required. Download the file `MCR_R2014a_win64_installer.exe`. Exact name of the file depends on operating system you are installing to. Download the file to a suitable location (i.e your desktop or a temporary folder) and double-click it. Follow the instructions in Figures 1-4.

This step to install MCR Installer does only need to be performed once and should generally not be necessary when upgrading to a later version of the software.

Note: For some operating systems it is required to reboot the computer after installing the MCRInstaller. We therefore, **strongly** advise all users to reboot the computer after installing the MCRInstaller.

8.1.2 Installing Segment

Download the file (called something like `install_Segment_2px_Ryyyy.exe`, where `2px` is the version number and `Ryyyy` is the revision number). Place

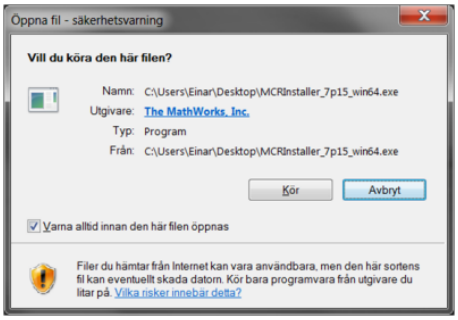

Öppna fil - säkerhetsvarning
Vill du köra den här filen?
Namn: C:\Users\Einar\Desktop\MCRInstaller_7p15_win64.exe
Utgivare: The MathWorks, Inc.
Typ: Program
Från: C:\Users\Einar\Desktop\MCRInstaller_7p15_win64.exe
Kör
Avbryt
Varna alltid innan den här filen öppnas
Filer du hämtar från Internet kan vara användbara, men den här sortens fil kan eventuellt skada datorn. Kör bara programvara från utgivare du litar på. Vilka risker innebär detta?

Figure 1: Click on `Run` or `Kör`.

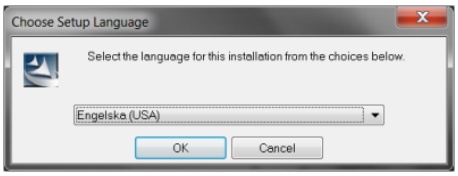


Figure 2: Click on `OK`.

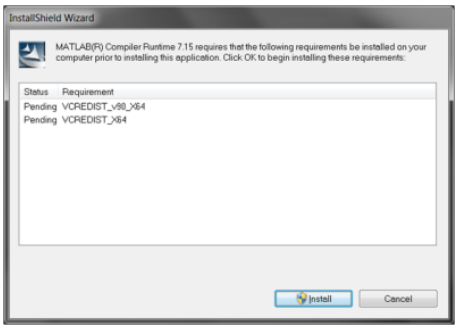

InstallShield Wizard
MATLAB(R) Compiler Runtime 7.15 requires that the following requirements be installed on your computer prior to installing this application. Click OK to begin installing these requirements:
Status Requirement
Pending VCREDIST_x86_X64
Pending VCREDIST_X64
Install
Cancel

Figure 3: Click on `Install`.

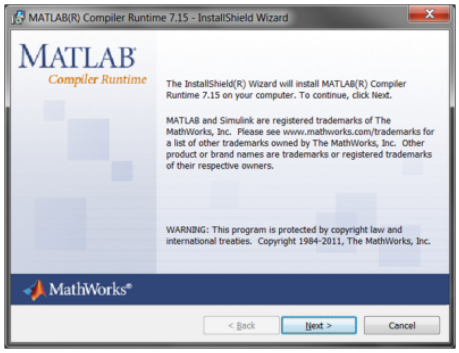

MATLAB(R) Compiler Runtime 7.15 - InstallShield Wizard
MATLAB
Compiler Runtime
The InstallShield(R) Wizard will install MATLAB(R) Compiler Runtime 7.15 on your computer. To continue, click Next.
MATLAB and Simulink are registered trademarks of The MathWorks, Inc. Please see www.mathworks.com/trademarks for a list of other trademarks owned by The MathWorks, Inc. Other product or brand names are trademarks or registered trademarks of their respective owners.
WARNING: This program is protected by copyright law and international treaties. Copyright 1984-2011, The MathWorks, Inc.
MathWorks
< Back
Next >
Cancel

Figure 4: Click on `Next`.

the file where you easily can find it (i.e your desktop). When downloaded, double click on the file, and follow the instructions. You will be prompted if you want to install the program to the default location (`C:/Program Files` or `C:/Program` depending on operating system language). One advantage of installing to another location, where you have write access, is that you can thereafter install upgrades without being logged in as local administrator.

8.1.3 Create shortcut

Place a shortcut to the file `C:/Program Files/Segment/Segment.exe` at your desktop. Note that depending on your system locale, or if you have installed Segment to a non-default location this path may be different. Creating this short-cut is done by using the standard Windows file explorer to find the file, then right click on the file and select the option Create a short-cut. Move the created shortcut to your desktop.

8.1.4 Notes for Windows Vista users

You will need to run the application in administrator mode the first time you run Segment since the first time Segment is started some files are extracted. This operation is blocked in user mode. The second time you run Segment you should be able to run in a user mode.

8.1.5 Network installation of Segment

For advanced users and system administrators, it is possible to make a network installation of Segment. Then you do not need to install MCRInstaller

on each machine that is used to run Segment. Make a network installation of MCRInstaller. How to do this shown in this document.

`www.mathworks.com/access/helpdesk/help/toolbox/compiler/f12-1000291.html`

Thereafter place Segment in a network folder, and make sure that each user can find `Segment.exe`.

8.2 Installation for source code version

Please note that currently is not Linux 32 bit supported, but Linux 64 bit are supported. We will at a later stage also support Linux 32 bit, but it is not easy trying to keep all platforms up to date.

Install Segment by:

1. Download .zip file (see download pages)
2. Unzip the file and store contents in directory.
3. Installation complete.

Starting by:

1. Start Matlab
2. Change directory to where you have unpacked Segment.
3. Type segment at Matlab command prompt.

8.3 License file

If you have received a license file (then your version is registered full version), then copy your license file to the same folder as where segment is installed. The license file is called `yourname.key` or `license.key`. If you do not have a license file then the program will run in 'Research only mode', fully functional where only a few options are disabled. You may then **not** use the software for commercial research or clinical routine.

8.4 Upgrading Segment

If your previous version used another MCR then you need to **first** replace your old Matlab Compiler Runtime. To see which version of Matlab Compiler Runtime is required, please see the table below.

Segment version	MCRInstaller
≤1.675	Matlab Compiler Runtime 7.6
1.8	Matlab Compiler Runtime 7.8
1.9	Matlab Compiler Runtime 7.15
2.0	Matlab Compiler Runtime 2014a

If you need to upgrade MCR, follow the installation instructions in section 8.1. It is **important** to uninstall the old MCR before installing a new one. When having problems installing or uninstalling the MCRInstaller, please consult Mathworks support pages, and search for `MCRInstaller`.

If you, as in most cases, do not need to upgrade MCR, simply download the Segment installation file and double click on it to install it, as described in section 8.1.2.

8.5 First time running Segment

Doubleclick the file `C:/Program Files/Segment/Segment.exe`, or your shortcut to it, to start the program. The first time it is started, it runs a setup process which can take a while, so be patient. To complete setup, set preferences and window positions as described in Sections 8.5.1 and 8.5.2.

8.5.1 Setting preferences

It is recommended to set the preferences of which folders to use to avoid browsing each time you want to load or save a file. It is invoked by using the Preferences on the main menu. Set `Data`, `Export` and `CD` folders.

The preferences are saved as a file `.segment_preferences.mat` in a folder that can be accessed by selecting Open Folder with Log Files from the Help menu. It is possible to customize a set of default preferences for every new user of a Segment installation by copying the preferences file to the Segment main folder and renaming it `default_preferences.mat`. This preferences file will then be copied to the preferences path of every user that does not

already have preferences saved.

Further details on how one customizes Segment is given in Customization Chapter in Segment Reference Manual.

8.5.2 Setting window positions

The position of the main window for Segment can be set by dragging the window to an optional position and size. The size and position will be saved so that next time Segment is launched the same position will be used. The window position can also be saved for the file loader, patient database module, PACS connection module, general segmentation module, fusion module, SPECT module and strain module. This feature is under development and eventually it will be possible to set the position for all windows, until then windows will pop up as an overlay in the middle of the window from which it was launched or in the middle of the main Segment window.

In case where one have switched to another monitor Segment may move outside the screen. In this case you could press `Shift-Ctrl-R` to reset GUI positions. This is also available under the File menu.

8.5.3 Patient database

We recommend that you start by using our example patient database. Download the file `Patientdatabase.zip` from Medviso AB homepage (http://medviso.com/download2/). The file is quite large (1.4 GB). Unpack the file and place the contents in a folder. It is recommended to place it in a subfolder where Segment is installed). In Segment you need to set the location of the patient database. Click on `Preferences` and click on `Advanced System and DICOM Settings`. A new user interface appears and click on `Database Folder`, select the folder where the file `patientdatabase.mat` resides.

8.5.4 PACS connection

Setting up PACS connection and Segment Server usually requires help from your local PACS support, and we recommend that contact us to setup a telephone / web-based video conference to make this process as smooth as possible. The Database and PACS connection manual and the Sectra PACS plugin manual is found at Medviso AB homepage

(http://medviso.com/products/cmr/resources/). The Sectra PACS plugin may require additional Microsoft Visual C++ components that can be downloaded from Medviso AB homepage (http://medviso.com/download2/).

8.6 Uninstallation

Essentially the uninstallation is similar for all versions.

8.6.1 Uninstalling for Windows

There is currently no uninstallation software available. Remove all files in the folder `C:/Program/Segment` or `C:/Program Files/Segment`. User preferences are stored in the `Application Data` and the subfolder `Segment` under each user account (Windows). To uninstall the Matlab Compiler Runtime, use the Windows functionality Install or Remove Programs in the control panel menu.

8.6.2 Uninstallation for source code

The uninstallation for the source code version is trivial, simply delete all Segment related files.

8.7 Trouble shooting

The absolutely most common problem is the failure to not login as a local administrator of the computer. The second most common mistake is not to read the installation instruction provided in this user manual or on the homepage.

To trouble shoot the installation you can see if the Segment installation program actually was successfully started by checking for the existence of `.log` files. Segment creates a log file during installation, this file is stored in the user folder (i.e `Documents and Settings/Username` and `Application Data` and the subfolder `Segment`. Note that this folder by default is hidden. If you have problems installing Segment, please send this log-file to `support@medviso.com` together with a description on what problems where encountered.

9 Loading Image Stacks

The best method to load and manage studies is by using the Patient Database Module, described in Segment Database Manual. For clinical use, we discurage the direct use of the DICOM loader since this is a sub optimal workflow in the clinical situation, instead please look at the Segment Database and PACS connection Manual.

The program can read DICOM, and also an internal file format. The internal file format (called `.mat` files) has the advantages that one file may contain several image stacks along with object contours and measurements, and it is also much faster and easier to load compared to loading DICOM files.

It is highly recommendable that when an image stack has been loaded from DICOM files to save the image stack(s) to the internal file format. This makes it then much easier to go back and reanalyse datasets if necessary. Note also that the internal file format requires much less storage space that the original DICOM files, mainly due to cropping of the images and to lossless compression.

How to browse your DICOM data in the easiest way is described in Section 9.1.6.

The file loading dialog box is started from the main menu, under File, or by clicking on the icon , or by pressing `Ctrl-O`. This brings up the file loader GUI shown in Figure 5.

The file loader process the selected directory and its subdirectories to find the number of files in that directory. Since this process takes some time this operation is cached, and creates a file called `folders.cache`. To recreate the cache, press . When reading from a CD-ROM it is recommendable to copy the CD-ROM to your hard drive if you will load most of the files on the CD-ROM, since random file access from CD is very slow and caching is not possible. For further details on how to import DICOM CD-ROM's, see Section 20.5.

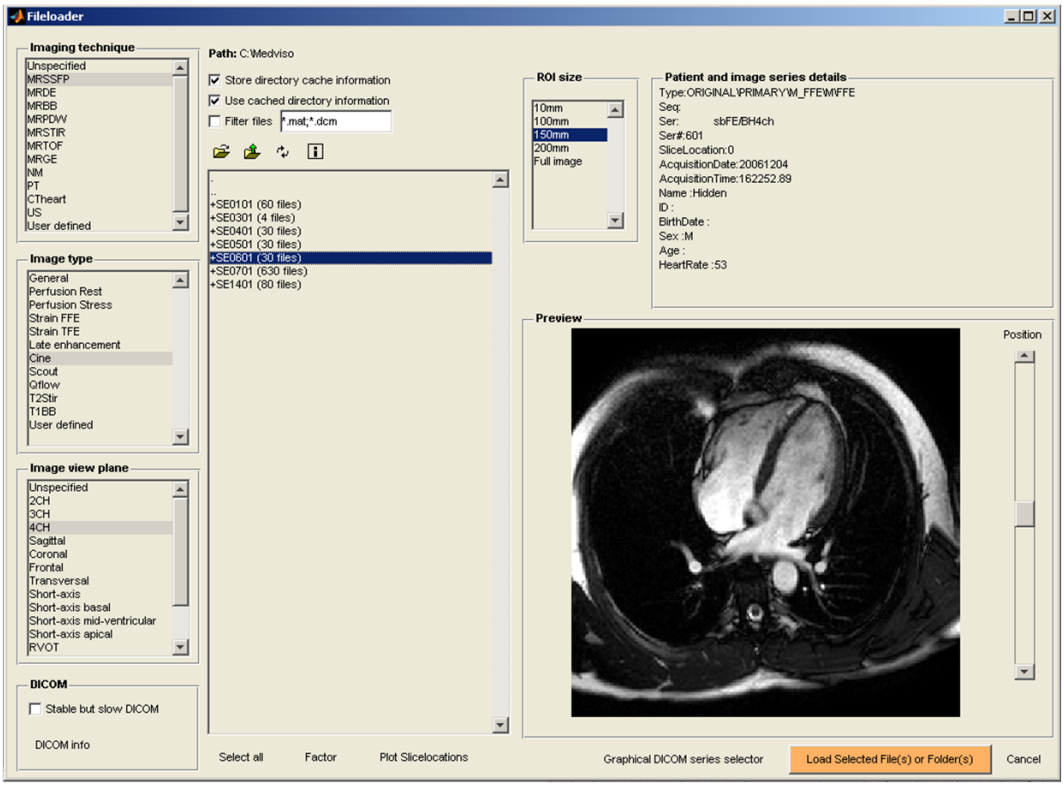


Figure 5: File loader GUI.

9.1 Loading DICOM files

9.1.1 Loading DICOM files

When loading MR DICOM files Segment assumes that the files are sorted so that each image series is stored into one folder. Each folder may then contain one or many DICOM files. This is illustrated in Figure 6.

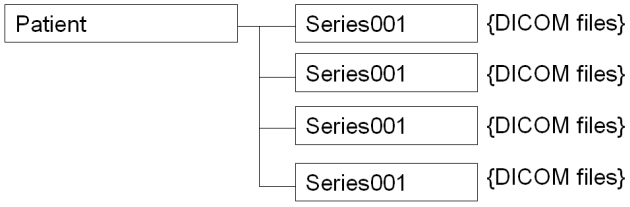


Figure 6: Files needs to be sorted so that each image series are stored into a separate folder.

If the files are not stored in this fashion then there is a sorting utility available described in Chapter 20. DICOM is an loosely structured file format and direct reading from DICOM files is slow. Currently the use of meta DICOM files is not supported (the DICOMDIR file is simply ignored).

9.1.2 Loading SPECT DICOM files

When loading SPECT DICOM files Segment assumes that the files are reconstructed into a short axis stack.

9.1.3 General loading DICOM files

You can either load each image series at a time or use a graphical tool to select what image stacks to load. The graphical series selector is described in Section 9.1.6. To load on image series at a time, start by selecting one folder. To go up one directory level double click on .., or click on the icon. To more easily get to a different folder, click on the Browse pushbutton. To go down one directory level double click on the folder name. Once selected one folder containing DICOM files a preview of one file in that folder is shown. To load the complete image stack, perform the following steps:

- Start by selecting the imaging technique in the top left corner of the GUI. The imaging technique sets the default segmentation parameters, and it is crucial that you select the correct imaging technique. For many scanners and sequence types this is identified automatically.
- When a valid file/folder is selected a preview of that dataset is displayed. Patient details and acquisition time are also shown.
- It is recommended, but generally not required to select `Image Type` and `Image View Plane`. This tells Segment what kind of image it is. This might be required for future analysis in some applications. It is also a good idea to label image stacks upon loading when for instance doing stress analysis to be able to safely differentiate baseline from stress exams. For research purposes it is possible to set free text name as `Image Type` and `Image View Plane`.
- Select the desired region of interest size. Usually for normal hearts 100mm is sufficient to cover the left ventricle. Enlarged ventricles will need 150mm or even more.
- Click Load to start the loading process. This brings up a red box in the preview image. Position this box with the mouse and left click to start the loading process. If you want to use a different size of ROI right click to abort loading operation. Then click again on the Load button.
- Once positioned the box, left click with the mouse to start loading the files.

Once all image files are loaded a dialog box opens where you need to confirm voxel spacing and timing details. How Segment interprets the DICOM information to calculate these parameters is described in Section 44.3. For users that do not use images from the three major vendors Siemens, Philips, or GE should read this section. Further technical details about how Segment interprets the DICOM files are given in the Segment Technical Manual.

If heart rate is not present in the DICOM file Segment tries to guess that based on the time increment and the number of time frames to get R-R interval. This will fail if your image sequence is for instance one image every heart beat.

9.1.4 Tips and tricks

Often the files are not stored exactly as prerequisited above, then there are many tips and tricks available.

- You may select several subfolders. Then the program loads all the files in the subdirectories. Each subdirectory must have the same number of files. This is the case for old Siemens files and Bruker Paravision DICOM files.
- You may select what DICOM files to load directly. Note however that the files need to form a valid image stack and the result may be incorrect if slices are missing etc. When you do this, always ensure that the files are sorted properly.
- It is possible to preview different files by the `Position` slider.
- To get detailed information about DICOM tags in the files press DICOM info.

9.1.5 Loading images from CD

When loading images from a CD it is highly recommended to import the files from the CD to your image data directory. This is done by using the utility described in Section 20.5.

9.1.6 Graphical image series selection

The graphical series selector tool is shown in Figure 7. While moving the mouse pointer over the image series more information on each image series is shown in the top of the graphical interface. Select which image series to load with left mouse button. Image series outlined in yellow are selected. It is also possible to group image series to one image stack. Image series that are to be grouped are selected by holding down the `Shift` key while mouse clicking, or by using the middle mouse button. Thereafter, press the push-button Group Selected. Grouped image series are shown with a green outline. Multiple image stacks can be selected for loading or grouping by clicking and dragging over the selection. When finished selecting image series, press Load. To speed up the process this operation the generation of the thumbnails is cached.

Note that when using this tool to load the image, then there is no cropping of the images done, and that is highly recommended to crop the images during

the image analysis process. Also note that if multiple directions is detected in the dicom folder all the different directions are loaded as separate image stacks.

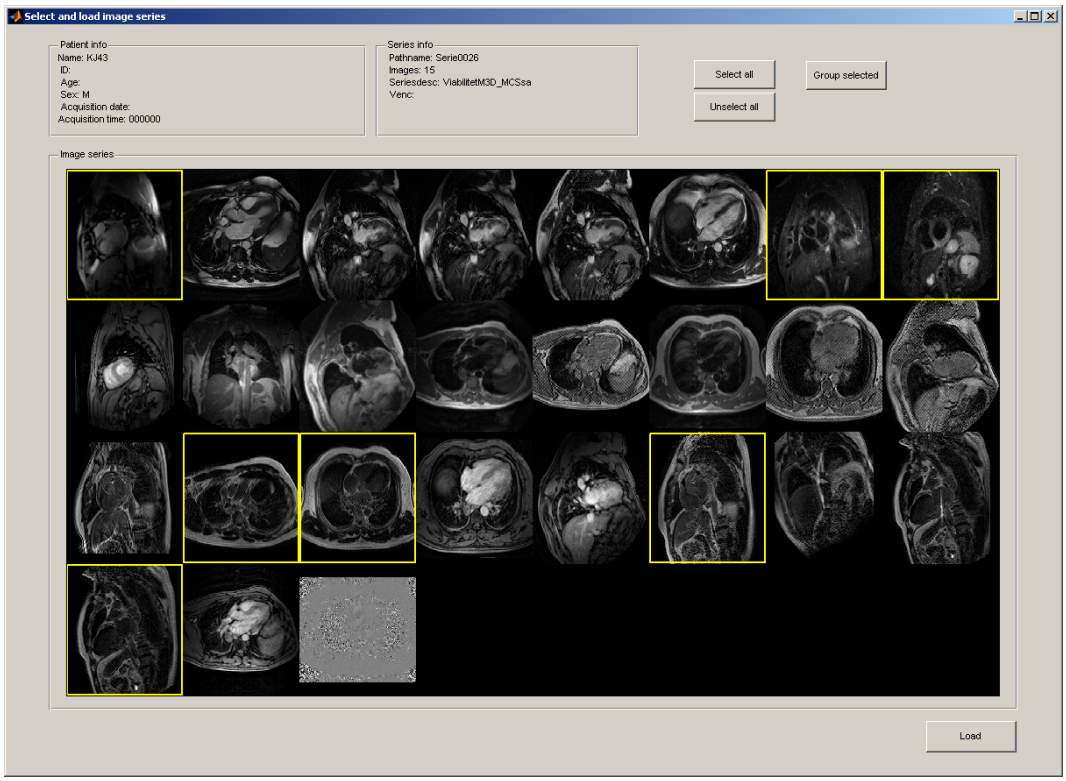


Figure 7: Graphical image series selector.

9.1.7 DICOM - details

First of all remember that DICOM is not a well defined standard. I have tried hard to make Segment to work with DICOM files from different imaging device manufacturers. It is currently tried on General Electric MR-scanners, Siemens CT/MR/PET, and Philips MR scanners, Bruker MR, Suinsa PET. Furthermore various PACS manufacturer might 'corrupt' the files in different ways.

The DICOM reader does not support JPEG encoded images, or big endian DICOM files. However, when images are imported into the patient database or sorted by the DICOM sorter they are converted on the fly and can be read by Segment DICOM reader.

There are some short cuts taken in the fast loader:

- The spacing in time is assumed to be equal between all frames when loading time resolved images. This may be violated if the scanner rejects some beats in a perfusion image serie for instance.
- The spacing in slice is assumed to be equal between all slices when loading image stacks with multiple slices.
- When you have loaded a rotated image stack you need to tell Segmentabout it. It is done under Image Tools and View Adjust and Image Details. A rotated image stack is a set of slices that are rotated around a central axis. Then subsequent analysis will assume that the data is a rotated image stack. When you view the data in single slice view ☐ a cyan line are drawn with the rotational axis indicated. To get correct volume estimates it is crucial that this line co-incides with the true axis of rotation. To achieve this you may have to flip the image stack, see details in Section 17.7.

9.1.8 Unstructured files

Some systems (Siemens depending on platform version, or how you do it or what PACS you are using) outputs files in a completely unstructured way (all patients and all time frames, and all slices) are mixed into the same folder. In Segment there is a sorting utility that can be accessed on the main menu that can sort the files. This is described in Chapter 20.

9.2 Matlab format - details

Internal format used by the program. The image needs the be stored in the variable `im` or `setstruct`, and must be in single precision format. The dimensions must be x, y, t, z. If you do not have time resolved data make sure to make the temporal dimension singleton, i.e. always put in a 4D-array. It is possible to also give dimensions, and patient specific information as well as a preview image. To learn about this, load an image stack from DICOM

images, and select Save Both Image Stacks and Segmentation As under the File menu. Then load the file in Matlab, and study the variables in the file. Details about the file format is given in the Segment Technical Manual.

10 Program Overview

This chapter provides an overview of the program. Another good method to get an overview of the program is to read the example in Chapter **??**. Yet a good method is to view the on-line video tutorials. The tutorials are available under the Help menu.

An example of the main graphical user interface is shown in Figure 8. The major portion of the user interface is occupied by a viewing area where multiple image stacks can be visualized side by side. The current active image stack is outlined with an orange thick line. To make another image stack active, simply click on the image stack with the mouse pointer. A thumbnail image is shown for each loaded image stack. To view an image stack drag the thumbnail down to the main viewing area. To scroll through the thumbnails either use the slider or press `Ctrl` while scrolling with the mouse wheel.

The upper right corner is occupied with a reporting panel where quantitative details about the current image stacks are shown. There are two rows of icons. The top row contains icons that applies to all loaded image stacks, whereas the bottom row contains icons to applies to the current active image stack only.

Middle right part of the user interface is occupied by a volume curve and a time indicator. This graph area shows left ventricle volume versus time (red), left ventricle muscle volume (green), papillary muscle volume (blue). One easy method to adjust the displayed time frame is by clicking in this graph. You can also interactively drag which time frame that is taken as end diastole (ED) or end systole (ES). Just above the volume graph a list box with assumed long-axis motion is located. In this example the long-axis motion is automatically calculated under the assumption that the left ventricular mass is constant over time. The program selects the long-axis motion amplitude that best fits this assumption. Note that this auto detect should be disabled when manually drawing contours. For further details, see Section 12.1.2.

If the checkbox ☒ Single frame is selected then segmentation and other opera-

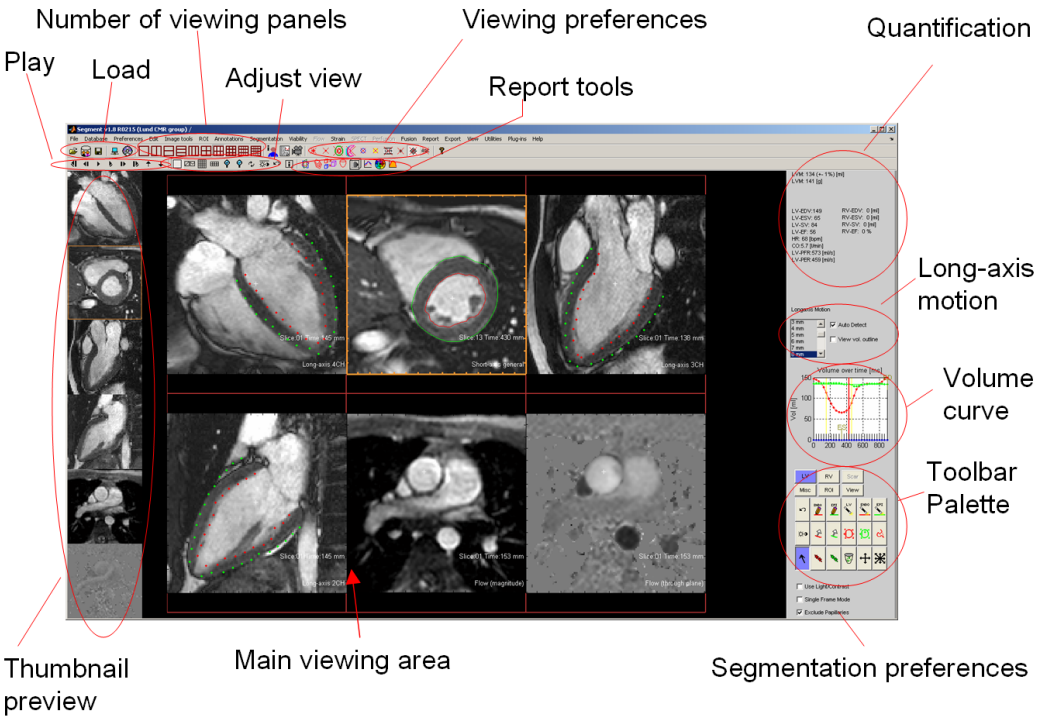
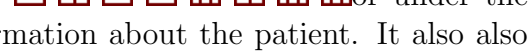


Figure 8: Main graphical user interface.

tions such as translate, scale, and delete are only applied to the current time frame. To further make the user aware of this change of behavior the box around the currently selected image panel turns to white when single frame mode is selected.

10.1 Viewing image stacks

To view a non visible image stack simply drag the thumbnail to an image panel. Right clicking on the thumbnails brings up a context menu where more options are available. To view all loaded image stacks press `Shift-A`. Only one of the image stacks are active at the same time. Around the active image stack an orange rectangle is drawn, both in the main image drawing area, and around thumbnail image.

Image stacks can be viewed in four different modes; one slice view, montage view, montage view in rows, and m-mode view. The different modes are selected with the icons (one slice), (montage or all slices), (montage view in rows), and (m-mode view). Each of the different viewing modes will be described in details below. It is possible to view the same image stacks in different viewing modes simultaneously. The number of image panels can be selected by the icons  or under the View menu. The icon views information about the patient. It also also possible to enter/adjust the patient information. Commonly this is used to add patient height to be able to calculate BSA.

The icon brings up an interface for saving and loading user specified views. This allows users to save their favourite combination of stacks to view for use with any image set. It is also possible to associate each saved view with a specified hotkey. When loading a saved view for a new image set, Segment automatically looks for the best matches among the current image stacks, taking into account such properties as image type, view plane, time resolution, etc. This interface also enables the user to save and load specific contrast/brightness settings, in absolute values, which can also be assigned a hotkey.

The section controls the visibility of pins, contours from other image stacks, endo / epicardium contours, region of interests, delineated infarct regions, measures and annotations, center point, and

image plane intersections, respectively. The icons and zooms in/out the current active image stack. The icon refreshes the screen which might be very useful since it also refreshed the GUI which under certain circumstances might 'hang' in case of calculations that went wrong. If the GUI seems irresponsive it is well worth to try refresh the screen. The icon resets the light/contrast setting. The icon automatically sets which sets contrast and brightness so that an upper and lower percentile of the intensities get saturated. The icon undo the latest contour editing command. The icon shows information about the current image stack.

10.2 Montage view

Figure 9 shows a screen-shot of the program in the most common view (montage view), selected by the icon . You can also switch between the montage view and the single slice view by using the hot key `v`. In the montage view all slices in an image stack are displayed. The slice(s) with a yellow box around are selected. Automated segmentation and many other operations are only applied to selected slices. Slices are selected by activating the tool , and by left mouse click on the desired slice and drag the mouse while the left button is hold down.

10.3 Montage row view

The montage row view is same as the montage row, but with the difference that the slices are shown to minimize the number of rows that are used to display the entire image stack.

10.4 One slice view

In one slice view only one single slice are shown at a time. You can then browse between slices by up/down arrow keys. Right and left keys displays next and previous time frames. In this view intersecting image planes that also are shown. The intersection are indicated with a white or an orange line. Orange line indicate intersection with the current active image panel. To hide/view the plane intersections use the icon . In this view intersections with contours drawn in other image stacks are also shown. For instance if the short axis stack is segmented the contour will also be visible in the long axis image. This is illustrated in Figure 10. This is very useful to delineate

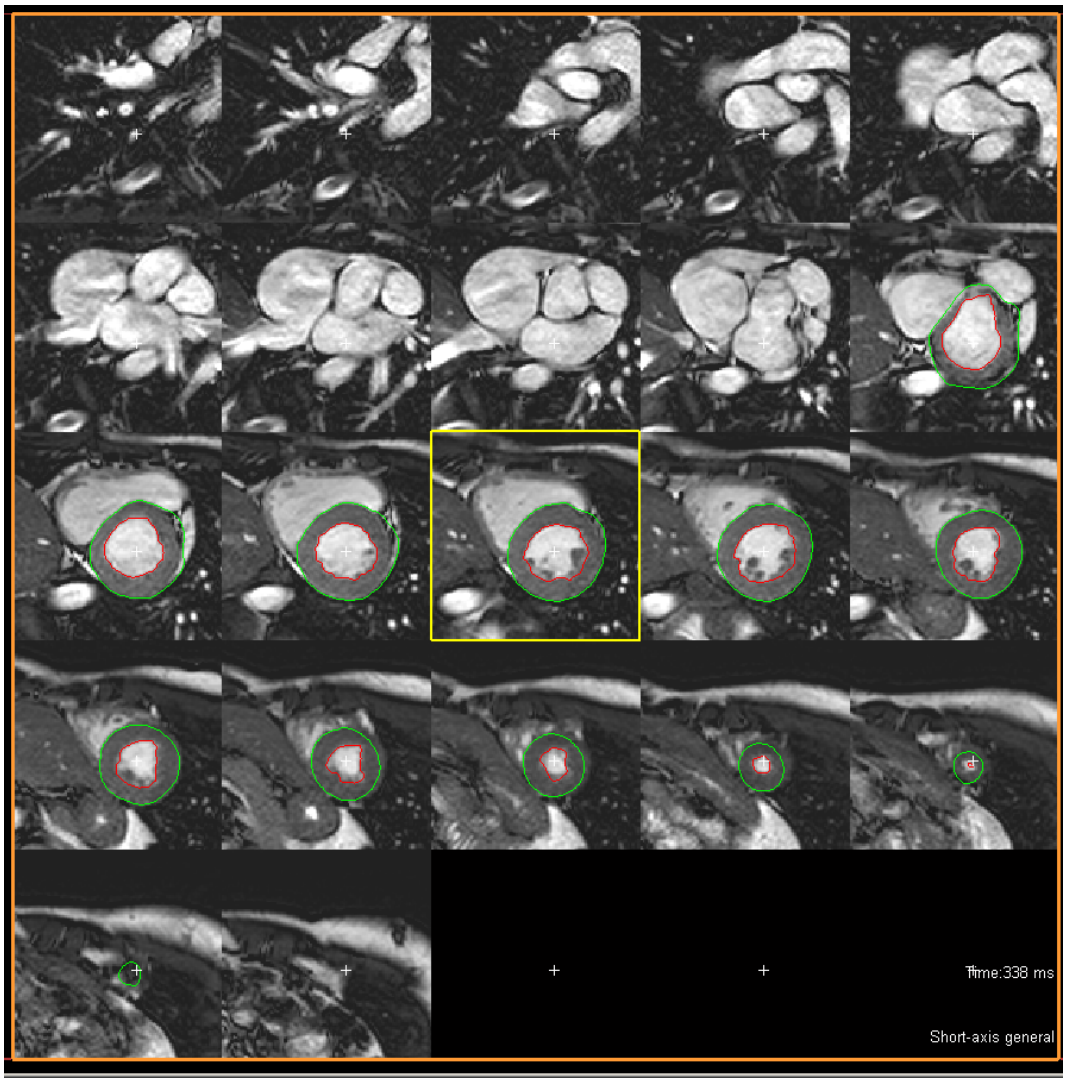


Figure 9: Screen-shot of the program showing an image stack in montage view.

structures that might be difficult to see in only one image plane. The contour intersections can be hidden by using the icon . The contour intersections are only visible in one slice view mode. Note that different breathing position may cause the image stack not to align properly.

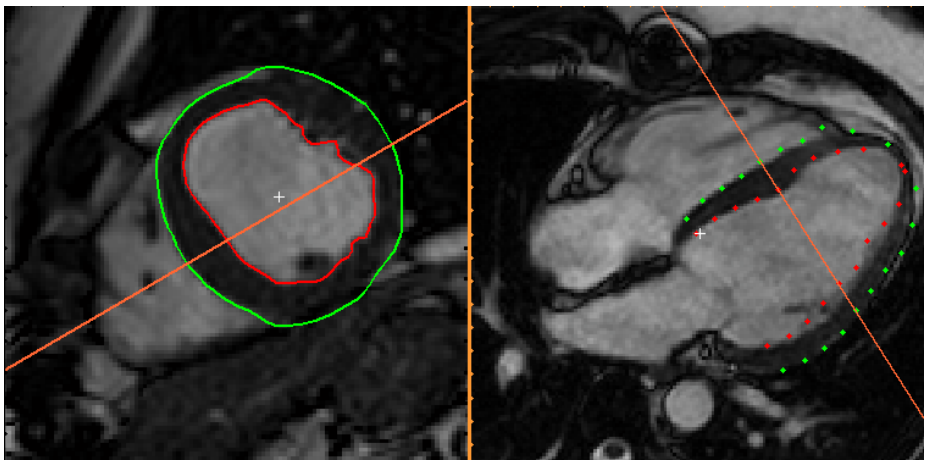


Figure 10: Contours are visible in other image stacks as dots. This is very useful to delineate structures that might be difficult to see in only one image plane.

10.5 M-mode view

Another viewing option is the (M-mode). Example of this view is shown in Figure 11. The viewing option is chosen by the icon .

In the image panel to the left one slice is displayed. To view a different slice use the up/down arrows on the keyboard. The right image panel a so called m-mode image is shown (the term comes from ultrasound motion-mode). This is a resampling of the left-image along the white line over time. The resampling line can be moved and angled by left-clicking on the blue circles and dragging the mouse while the left mouse button is hold down. Along the lines there are two callipers shown as a white cross. The same callipers are showed in the right image as vertical white dotted lines. Distance between

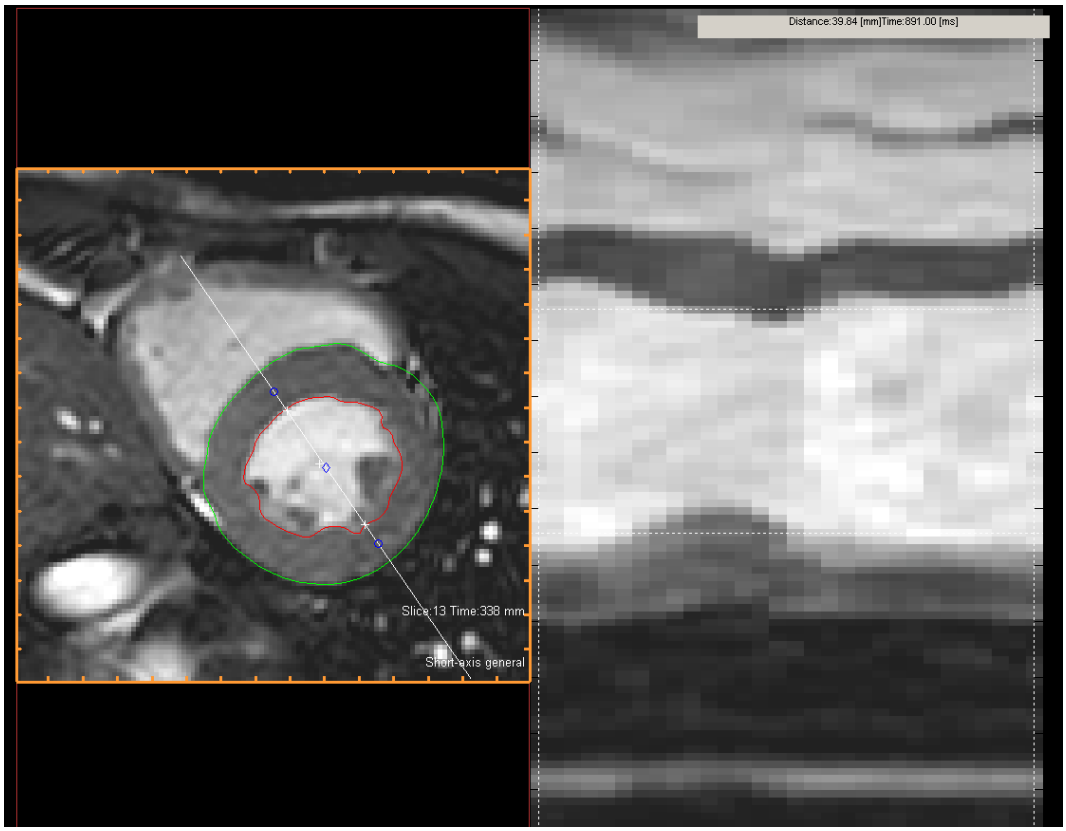


Figure 11: Screen-shot of the program showing an image stack in M-mode viewing mode.

the two callipers is displayed under the m-mode image. To measure time events two time bars are shown in the m-mode image. These can be dragged with the mouse, and the time between them is shown above the m-mode image.

This viewing mode can also be used to make measurements. An example on how this can be used is given in Section 12.1.2.

10.6 Viewing velocity encoded image stacks

For velocity encoded images it is possible to view both the magnitude image and the corresponding velocity encoded image(s). In the thumbnails a white box is drawn around magnitude and phase image to indicate what image stacks belong to each other. For more details see Chapter 23, Flow Analysis.

10.7 Playing images as a cine-loop

In the main icon toolbar the controls what time frame of the image sequence is displayed. The icon (`Shift-left`) shows previous frame but applies to all visible image stacks. It displays the previous frame for the current image stack, and tries to find the corresponding time frame for all image stacks. The icon (`left`) displays the previous time frame for the active image stack. You can also use left arrow button. The icon plays the active image stack sequence as a cine loop. The icon (`right`) shows the next frame for the active image stack. You can also use right arrow button to show the next frame. The icon (`Shift-right`) performs the same operation as , but forward in time instead. Control and arrow keys show previous/next frame for all image stacks. The icon increases the playback speed, and decreases the speed. Another convenient method to quickly move between time frames is by clicking in the volume graph. Here you can also interactively drag which time frame is used as end diastole (ED) or end systole (ES). You can also switch between systole and diastole by using the hot keys `d` and `s`, respectively. Yet another way to scroll between time frames is to use the mouse wheel and at the same to press `Shift`.The icon allows the user to perform manual delineations while the current slice is played. This is very useful for a better understanding about for instance the papillary muscles.

10.8 Synchronizing image stacks

It is often required to synchronize image stacks in time and slice. This can be done by using the Shift-key. Shift-left/right key shows previous/next frame and synchronizes all visible image stacks in time. For image stacks that have different number of time steps the nearest time frame is shown. `Shift-S` and `Shift-D` toggles between systole and diastole in all visible image stacks.

10.9 Loading and storing images

The top left section of icons contains functionality to load and save image data. The first icon opens a file loader GUI described in Chapter 9. The second icon opens the patient database described Segment Database User Manual. The third icon saves all the loaded image stacks to one file. The fourth icon opens a connection to a PACS server, see Segment Database User Manual.

10.10 Tool palette

The tool palette is located at the lower right corner of Segment main graphical user interface. The tool palette have several modes in which different tools become available. The current mode is indicated as black text on blue background. The current active tool is indicated by displaying the tool in a darker gray color. Generally, with few exceptions all functions in the program only applies to selected slices. Selected slices are indicated with a yellow box in the montage view. The functionality of selecting slices can only be used in the montage view. An alternative to select slices is to use the short key `Ctrl-A` that selects all slices. To pan the image use the tool and move the mouse.

There are some general tools that are present in all tool modes, and these are:

	Select slices or image stacks. This is the default tool.
	Translate ROI's and contours or the whole image if no ROI or contour was clicked.
	Change the size of ROI's and contours.
	Undo last contour edit command.
	Adjust brightness and contrast. Hold down the mouse button and move left/right to adjust contrast and up/down to adjust brightness of the current image stack. By holding down the `Shift` key while pressing the mouse button, the adjustments also affect every other image stacks in the current view, and sets the absolute values of their contrast and brightness to be equal to those of the active image stack. Contrast and brightness of the current image stack can also be adjusted without first clicking the icon, by instead using the middle mouse button.

10.10.1 Left ventricle tools

The left ventricle tools are shown in Figure 12. Colors are used to indicate endocardium (red) or epicardium (green).

On the first row (from left to right); is used for an interpolated contour mode to click out points to control the endocardial contour. To close the contour and interpolate a line between the points, shift click in the image. The points can interactively be dragged. The second tool is used to manually draw the endocardium. The third tool is to automatically refine the endocardium. The fourth tool puts endocardial pins that guides the automated segmentation. The fifth tool is to interactively drag the endocardium with the mouse.

Figure 12: Left ventricular toolpalette.

On the second row is the same as the first row except that the tools applies to the epicardial contour instead of the endocardial contour.

On the third row (from left to right): The first icon automatically segments both endocardium and epicardium of the left ventricle. You need to ensure that the center '+' is in the middle of the ventricle and that all slices that covers the left ventricle are selected, see Chapter12. The second icon automatically segments the endocardium in the selected slices. The third icon automatically segments the epicardium of the selected slices. The fourth icon attempts to remove the papillary muscles. This can be use multiple times to successfully remove them. The last icon deletes the segmentation in the selected slices.

Generally, the space key can be used to toggle between the endo and epicardial tool counterparts.

10.10.2 Right ventricle tools

The right ventricle tool palette is shown in Figure 13. The icon is used to click out points in the interpolated contour tool for the right ventricle endocardium, and is used for the epicardium, respectively. The icon is used to manually draw the right ventricle (RV) endocardium. The icon is used to automatically delineate the RV endocardium. Note that the RV tool is not as automated as the LV tools. The icon is used to refine the RV endocardium. The icon is used to put RV endocardial pins for guiding the automated RV segmentation. The icon is used to manually drag the

RV endocardium. The icon is used to manually draw RV epicardium.

Figure 13: Right ventricular toolpalette.

10.10.3 Viability/Scar tools

The functions described in this section is in US only for off label use and for investigational use.The viability tool palette is shown in Figure 14.

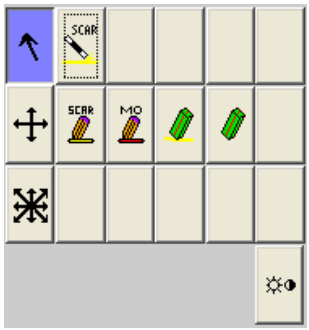


Figure 14: Viability toolpalette.

The icon is used to automatically delineate infarct region on MR delayed enhancement images. The icon is used to manually delineate infarction. The icon is used to manually delineate regions with microvascular obstruction. The icon manually removes infarction. The icon erase manual corrections of infarction. The show the manual interactions and regions of microvascular obstruction you need to press the key `o` to toggle the display.

10.10.4 Miscellaneous tool mode

The miscellaneous tool mode is shown in Figure 15.

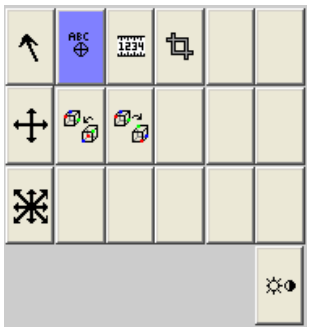


Figure 15: Miscellaneous mode toolpalette.

The icon is used to place annotation points. The icon is used to make length measurements. Left click with mouse at the starting point and hold mouse button down and move the mouse to end point. It is possible to interactively drag and refine measurements later. The icon is used to crop the current image stack. The icon is used to automatically crop all image stacks to focus on the heart, in order for it to work properly at least one time resolved short axis image stack is required. The icons and are used to rotate the image stack in 3D space. The icon allows you to find positions in 3D space for all visible image stacks.

10.10.5 ROI tool mode

The toolpalette for region of interest analysis (ROI) is shown in Figure 16. The first tool is used to manually delineate region of interests. The icon is used to automatically outline a vessel from scratch. Before using this place the center point (+) in the middle of the vessel. The icon refines a vessel. This is done in all time frames if the checkbox is unchecked. The icon copies the ROI contour to next time frame and refines it. The icon tracks a ROI over the entire cardiac cycle. The icon selects current color to use to draw ROI's. The icon is used to name the current ROI.

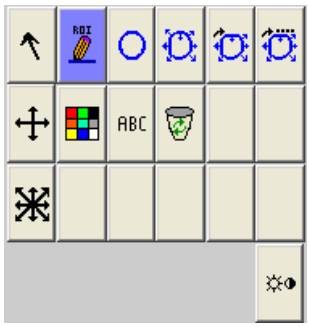


Figure 16: Region of interest mode toolpalette.

10.11 View tool mode

This mode is useful for quickly picking different views of the image stacks. The toolpalette is shown in Figure 17.

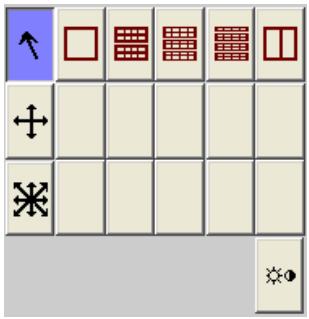


Figure 17: View mode toolpalette.

The first icon shows cine images, shows both cine images and the corresponding short axis delayed enhancement images, shows cine, delayed enhancement and perfusion images, shows a stress display, shows a flow view with a magnitude and a phase contrast image to the right. This mode is subject for future improvements.

10.12 General view and reporting functionality

The report tool creates a full text and graphical report of all the measurements for all image stacks. The icon starts a movie recorder that allows to

store an image stack as an `.avi` movie. It is also possible to directly export a movie under the Export menu.

There are seven tools available to visualize or handle image stacks. Each of these starts separate graphical user interfaces to view and manipulate image data. They are all available as icons on the main menu. The icon starts the general segmentation tool described in Chapter 15. The icon starts a tool to do multiple planar reconstructions, described in Chapter 30. The icon starts the Image Fusion Module. The icon starts a three dimensional visualization tool, and an example of a such visualization is shown in Figure 18. The icon starts a volume rendering tool. This tool is under development and currently unavailable. The icon starts a tool to do regional wall motion per slice analysis described in Section 26.2. The icon starts a tool to do bullseye visualization of wall motion and infarct parameters. The last icon starts flow analysis tool, described in Chapter 23.

11 Image settings

11.1 Manually set image description

To manually set the image description for an image stack, right click on the thumbnail for the image stack. Then select Select Image Description in the context menu and define the image description.

11.2 Image description upon loading

The image description is automatically set in the loading process by comparing information from the DICOM tags with the information in the text file `imagedescription.txt`. You can manually update the text file to improve the automatical definition. This is done by open the text file, which is found in the folder where Segment is installed. Then manually update the text file according to the structure as defined in the first row in the text file and store the text file.

12 Segmentation of the Left Ventricle

Before starting to describe segmentation of the left ventricle it is of importance to define what do we consider as the left ventricle.

12.1 Definition of the left ventricle

At a first thought it seems very easy to define what part of the heart should be included in the left ventricle. At a second thought the definition needs to be practical and repeatable. In the program the following decisions have been made.

12.1.1 Papillary muscles

By using the automatic LV segmentation algorithm, the papillary muscles are removed as much as possible (even if they are attached to the wall). Details on how to manually include/exclude the papillaries are given in Section 12.3.

12.1.2 Mitral annulus

Long-axis motion of the left ventricle is a very important component to achieve correct ejection fractions, and volumes. Long-axis motion is accounted for in the automatic LV segmentation algorithm. The long-axis motion direction is assumed to be orthogonal to the slice direction. The long-axis direction is shown in Figure 18. In the most basal LV slices the algorithm defines the LV segmentation with the long-axis motion in mind.

12.2 Start the segmentation process

Before starting the automatic LV segmentation process, make sure that the basal-apex orientation is correct. The most basal slice should be in the upper left corner. If not then select Image Tools→Flip z and x, as described in detail in Chapter 17. Also make sure that correct `Image Type` is selected when loading the image stack (MR SSFP, CT...). This can also be set afterwards by right-clicking on the image stack thumbnail image and select `Set Image Description`. If the checkbox ☒ Single Frame Mode checkbox is checked, a

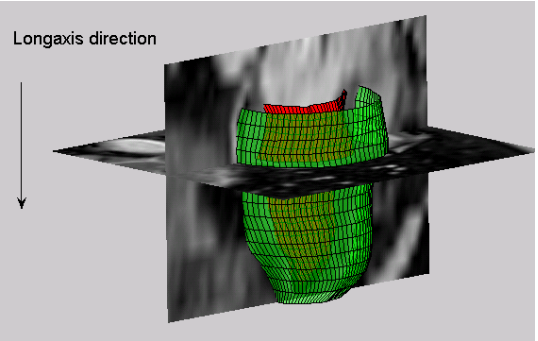


Figure 18: Three dimensional view of the left ventricle showing the long-axis direction.

message box questioning if you would like to perform LV segmentation in all time frames is asked. It is recommended to do the LV segmentation in all time frames since this leads to better conditions for the segmentation algorithm. However, you can select to only perform the LV segmentation in the selected time frame.

In order to start the segmentation process click on in the LV mode. A new interface is open, according to Figure 19, where you select the most basal slice and the most epicardial apical slice of the LV. The basal limit should be the most basal slice that have left ventricular myocardium at least in some part of the heart cycle. If long-axis image stacks are available, the slice selection can be reviewed in the long-axis views. In order for Segment to find the long-axis image stacks, the `Image View Plane` have to be defined as `2CH`, `3CH` or `4CH`. The `Image View Plane` is defined by right click in the thumbnail preview and select `Set Image Description`. The next step is to ensure that the LV center cross is correctly defined in the middle of the LV lumen. This is done by review, and if needed adjust, the orange cross in the short-axis view. The center cross should be in the middle of the LV lumen for the midventricular slice and the placement in the basal and apical slices is irrelevant. After the selection of LV slices and definition of LV center, the automatic LV segmentation is started by click on Start LV segmentation. The final result from the automatic LV segmentation algorithm is then displayed in the main interface for Segment. If needed, manually adjustment of the LV segmentation is performed in the main interface according to Section 12.3.

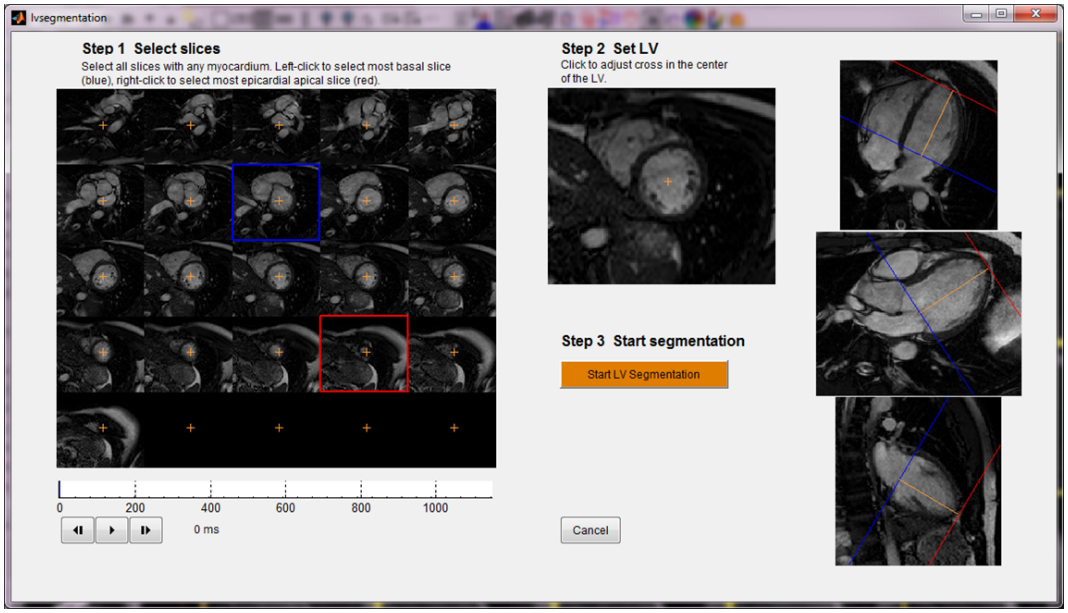


Figure 19: Interface for LV analysis.

12.3 Edit the segmentation result

Unfortunately the segmentation result is not always as one would desire. We have done as much as we possible can to implement and design a segmentation algorithm that is robust and accurate, but despite that the algorithm do fail in certain cases, and especially on the epicardial contour.

There are many implemented methods to manually edit the segmentation result. Different methods are good in different situations. I recommend to learn them all, and by experience learn in what situations the different types of manual interaction works best. If you experience that editing is a cumbersome task, then you are probably doing it the wrong way.

When the segmentation fails completely, please check the following items:

- Double check that you selected the correct Image type (MR Gradient echo, MR SSFP, CT contrast etc) when you loaded the data. This is very important for the segmentation result. Right click in the thumbnail preview and select `Set Image Description` to do this.

- Double check that correct slices are selected for the LV segmentation and that a good LV center point is chosen.

There are several methods to manipulate the segmentation result. Each method have different applications where they work better, and it is a learning process to learn which tool to use in different situation.

12.3.1 Undo segmentation

To undo the latest segmentation operation select undo from the tools menu, or using the undo icon , or using the hot key `Ctrl-Z`.

12.3.2 Refine segmentation

Refine runs the segmentation algorithm a few iterations, and thus further refines the segmentation. This functionality is chosen by the two icons and for endocardium and epicardium, respectively. Note that the optimization is only run for the selected slices.

12.3.3 Propagate segmentation

An efficient way of handling erroneous slice is to copy the LV segmentation results from an adjacent slice. This is especially efficient in the more basal slices. The program copies the LV segmentation in selected slices and refines the position of the contours by a few iterations. To propagate a segmentation forward in time one time frame, press Ctrl-F. If the endocardial pen is selected then the endocardium is propagated, and if the epicardial pen is selected , then the epicardium is propagated. The hot key Ctrl-F also applies to ROI's if the ROI pen is selected. You can also use the tools or to propagate the endocardium or epicardium, respectively.

12.3.4 Expand or contract segmentation

If the shape of the contours is satisfactory but are inside or outside of the myocardial border, the tools , , or can be used to expand or contract, respectively, the contours. The tools are applyed on selected slices and expand or contract the contour in a relative manner. If the checkbox ☒ Single Frame Mode is checked, then the tool is only applied in the current time frame, otherwise in all time frames.

12.3.5 Manually adjusting the contour by interpolation points

Manually correction of the contou by using interpolation points is probably the easiest way to make changes in the segmentation. This functionality is chosen by the two icons and for endocardium and epicardium, respectively. If there is LV segmentation in the selected slice, one left mouse click in the current slice will put interpolation points for the contour. If no LV segmentation is present in the current slice, a LV segmentation can be performed by the interpolation points by select or tool. Then add interpolation points by left mouse click and interpolate the contour by shift-click. The LV segmentation is then corrected by move the interpolation points by dragging with the left mouse button and hold it down. New interpolation points can be added by left mouse click in at the position where you like to add the point.

12.3.6 Manually drawing the contour

This functionality is chosen by the two icons and for endocardium and epicardium, respectively. Use the left mouse button and hold it down to manually draw the complete contour or correct an existing contour. If the checkbox ☒ Single Frame Mode checkbox is checked, then the segmentation is only performed in the current time frame, otherwise in all time frames. A quick method to toggle between drawing epicardium, and endocardium is to use the space button on the keyboard.

12.3.7 Translating the segmentation

The segmentation can be translated/dragged in each slice. This is done by using the icon in the toolbar palette. Note that the usage of this translation is especially useful in conjunction with the import segmentation option in the main menu. Then a segmentation from one imaging technology can be overlaid an image of a different image stack if they were acquired using the same coordinate system. A practical application is doing the segmentation on cine gradient echo or cine SSFP images and overlay that result over late enhancement images. Under the segmentation menu it is possible to translate/move selected slices towards the base/apex.

12.3.8 Scale the segmentation

In some slices, and typically the apical slices scaling the segmentation can be very effective correction. Scaling can be done with the tool. Scaling

can often successfully be combined with the refine operation.

12.3.9 Manually include/exclude papillary muscles

One approach to remove papillary muscles is to perform a few iterations with the refine tools for the LV segmentation according to Section 12.3.2. The papillary muscles can also be included/excluded in the LV segmentation by using the manual drawing tools according to Section 12.3.6.

12.3.10 Removing segmentation result

The segmentation result can be removed with the right mouse click pop-up menu (shown in the place pin section above). These function are also available in the main menu under Segmention.

13 Segmentation of the Right Ventricle

The right ventricle is much more geometrically complex than the left ventricle. The walls are much thinner and there are more and complex trabeculation. This is one explanation that there are currently in Segment no really good automated tools to do segmentation of the right ventricle. This will be improved in future versions of Segment.

Currently what is available are the same basic functionality as for the left ventricle. For the mid ventricular slices the automated methods (manual draw+refine can be used).

At the current stage we do not recommend to do time resolved segmentation of the right ventricle since the drawing and edit tools are so poor. We would the suggest to remove all RV segmentation except systole and diastole. An example of segmentation of the right ventricle is shown in Figure 20.

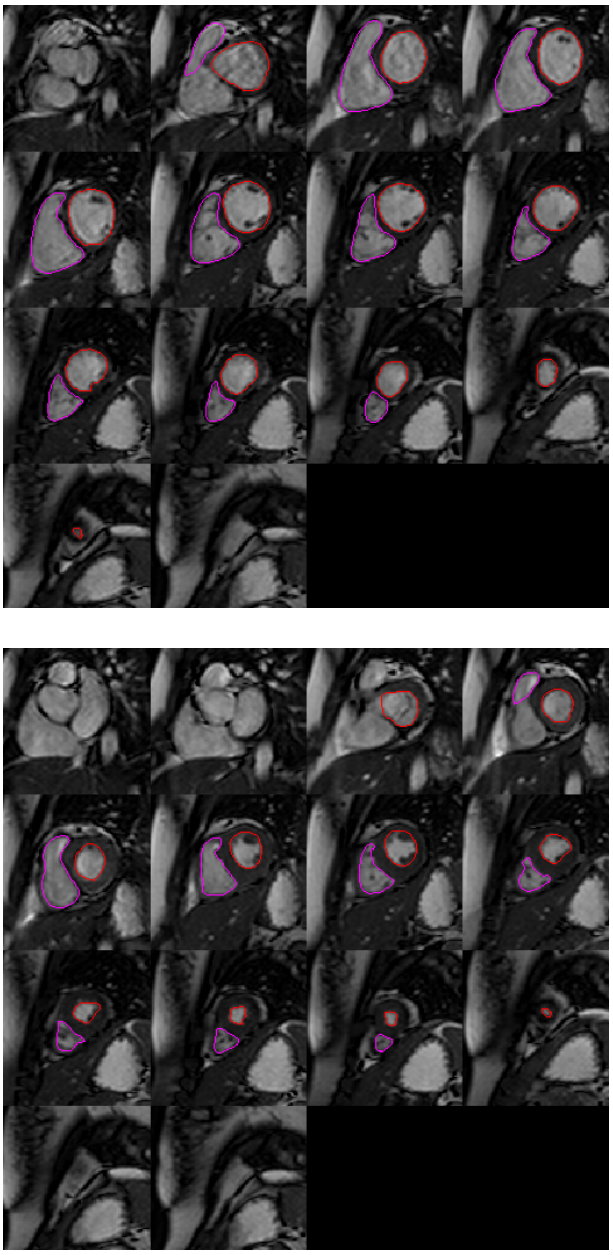


Figure 20: Top: Segmentation of the right ventricle in diastole in a short axis image stack. Bottom: Segmentation of the right ventricle in systole in the same short axis stack. Note the relative large long axis motion.

14 Segmentation of Long Axis Images

Segmentation of the left ventricle (as well as any other chamber) can be done by manually outlining the object in longaxis images. This is a fast alternative to manual drawing on short axis images.

Contours need to be present in at least two image stacks labeled 2CH, 3CH or 4CH to enable volume calculations. Please note that the image stacks needs to be labeled view the correct view. To label the images right-click on the thumbnails and select Set Image Description. Figure 21 illustrates the concept of segmentation in long axis images.

14.1 Click an image to show point location in all views

To provide a better estimation of the three dimensional volumes when drawing in longaxis images, there is a tool that allows the user to click an image to show the location of the clicked point in every active view. This tool is found in the Misc toolbox.

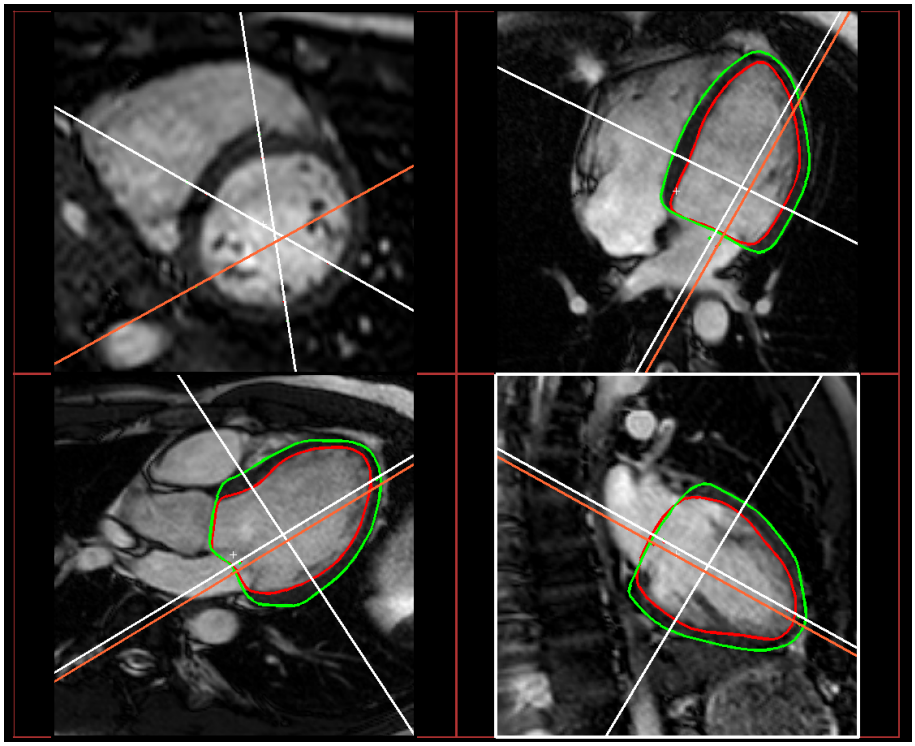


Figure 21: Illustration of the process of drawing segmentation in long axis images.

15 Segmentation of General Objects

The functions described in this chapter is in US only for off label use and for investigational use. This module is useful for delineating complicated 3D anatomical objects. Since it is less specialized than the segmentation of the left ventricle, it is less automated.

The functions described in this chapter is in US only for off label use and for investigational use.

Promising new techniques such as prototype based image segmentation [1] has been incorporated in this module, Section 15.9.

15.1 Viewing data

The graphical user interface is shown in Figure 22. There are three orthogonal views and one view of the speed image further described in Section 15.2.2. The slice position of the upper right image is shown as a red line in the two other slices. The leftmost lower image, and rightmost lower image are shown as green, and blue lines, respectively. When the selection tool is active then by left click in any of the three orthogonal views the postion of the image planes can be adjusted. There are four checkboxes that control how the data is displayed. When the checkbox ☒ as MIP is checked then the shown image is a MIP image (Maximum Intensity Projection). Note that contour overlay is not done in the MIP projection. The checkbox ☒ Interaction shows manual edits and region growing interactions. Placed seed points and added areas are shown in green and removed areas are shown in blue. The checkbox ☒ Selection shows the segmented object in red color. Finally, the checkbox ☒ Outline determines whether the object outline (displayed in yellow color) is shown or not.

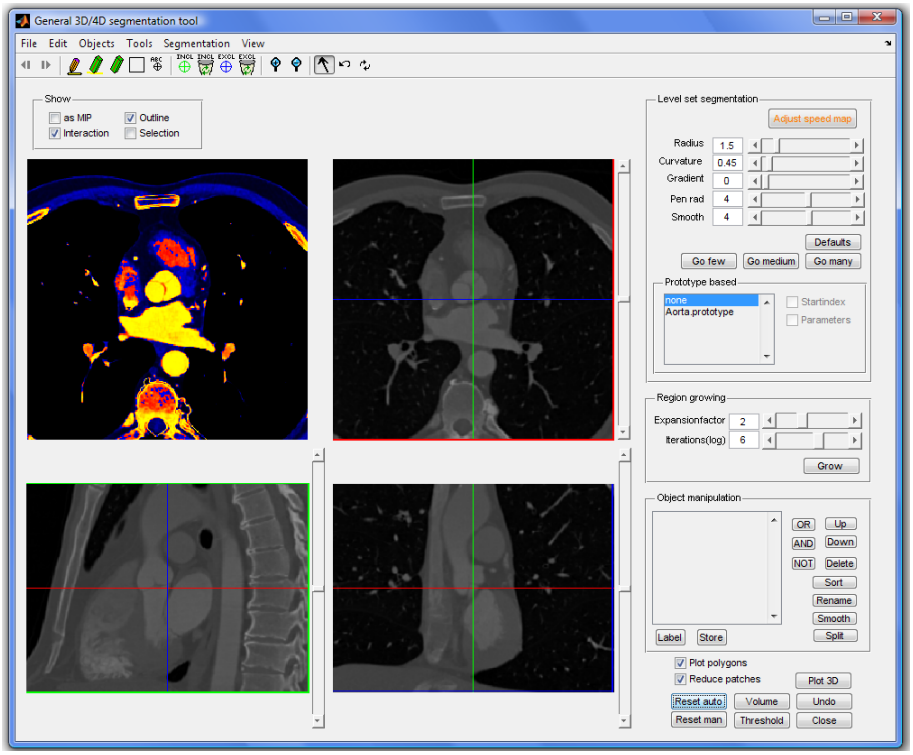


Figure 22: Graphical user interface for general object segmentation.

15.2 Level set segmentation

15.2.1 Algorithm

The algorithm is based on a very fast level set algorithm [2]. From a seed point or set of seed points the object is expanded outwards. The expansion is stopped at edges or regions with low signal intensities. The expansion is also penalized for large curvature, i.e. the algorithm favours object with low local curvature. The expansion (or contraction) is allowed to continue for a number of iterations. The key to the sucess of the algorithm lies in adjusting an appropriate expansion speed.

15.2.2 Optimizing expansion speed

Before adjusting the expansion speed you should draw some seed points. Image intensity for the seed points are used in the calculation of the expansion speed image, for details, see below. There is a separate graphical user interface to help adjusting the speed image calculation. This user interface is shown in Figure 23. In the upper left panel, an intensity histogram of the complete volume is shown. In the lower left panel a function that maps signal intensity to local expansion speed is shown. In the upper right image panel a magnitude slice is shown. Different slices can be selected by usage of the Slice slider. In the lower right image panel the corresponding speed image is shown. Bright red and yellow colors denote expansion, whereas dark and blue colors denote contraction. Four different speed mapping modes can be chosen; Gaussian, Positive slope, Negative slope and Prototype shaped. The Gaussian shape is useful when one want to delineate objects within a certain signal intensity range. One example is mapping certain Hounsfield units from CT images. In future versions of `Segment` it will be possible to store a set of speed mappings, and couple them to the normalized image values used in `Segment`. The Positive slope is useful to segment regions that are brighter than a certain image intensity, and the Negative slope is useful to segment regions that are darker than a certain image intensity. The Prototype shaped speed mapping mode is further described in Section 15.9. The mapping is 'translated' by adjusting the Offset slider. The default behavior is that the mean signal intensity is used as 'zero' level of the speed intensity mapping. This is useful since after selecting seed points only small adjustments of the Offset slider is the usually required. By unchecking the checkbox Intensity from seed as offset the 'zero' level will instead be 0.5. The slope of the map-

ping is adjusted by usage of the Width slider. When pleased with the settings on how the speed image is calculated press Dismiss.

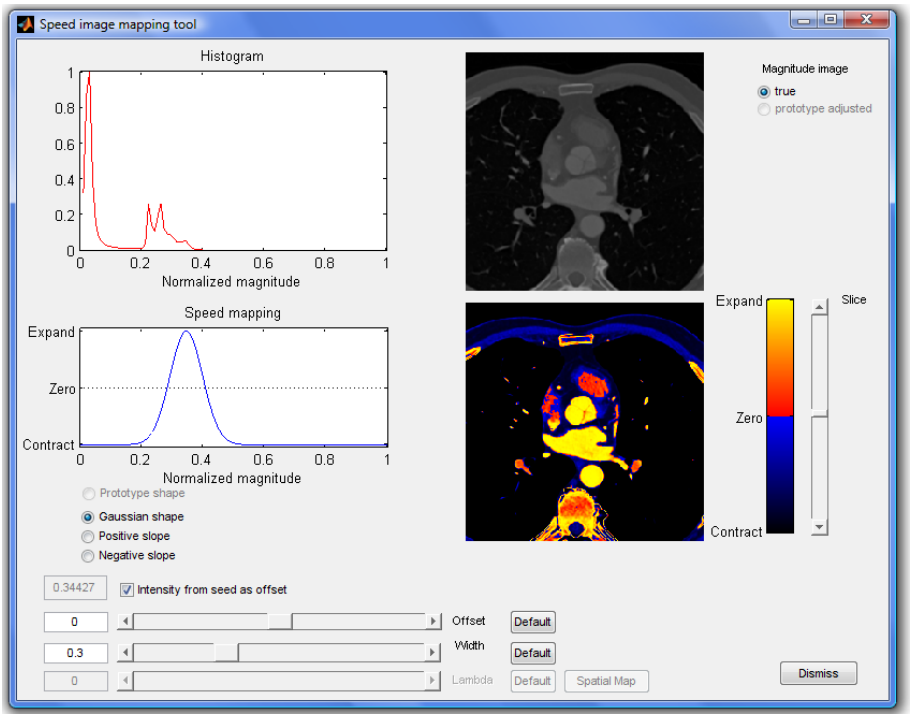


Figure 23: Graphical user interface to adjust speed image.

15.2.3 Start the segmentation tool

Start the segmentation process by first draw some seed points/regions by selecting the draw tool . The thickness of the pen can be adjusted by the slider pen radius. The pen draws a sphere of the radius set by the slider in all three or four dimensions, so you need to start to think and work three dimensionally. If the checkbox ☒ Manual interaction is checked then added regions with is colored in green and removed regions with the tool are colored blue. By using the tool it is possible to remove user interactions created with the two tools and , respectively.

After drawing some seed points adjust the speed image such as the desired object(s) is shown in a red or bright yellow color. This is described in detail in Section 15.2.2 above. The user interface is started by the Adjust speed map. This adjustment is rather critical for the final result, so do this step with care.

Start the segmentation algorithm by the pushbutton Go few (iterations). The smoothness of the final segmentation result can be adjusted by changing the algorithms penalty for curvature. This is done by the Curvature slider. Note that you can also smooth the segmentation result. This is described in detail in Section 15.6. The slider Radius control how large volume is used for curvature calculation. The slider Gradient control how sensitive to boundaries in the image the algorithm will be. Large value means the algorithm is more likely to stop expanding at boundaries. If thecontour of the object expands as planned then continue with Go medium or Go many if necessary.

15.3 Manual interaction

You can manually edit the result by using the drawing tool or the removal tool . For each voxel in the image volume manual corrections can be of three kinds; no change, i.e. no manual correction, or pixel included, or pixel removed. By using the tool ☐ it is possible to draw a box in any of the three orthogonal views. This box can then be filled so that it is avoided in the delineation or included in the delineation. This is very useful when one want to manually exclude large portions of the image stack from the segmentation. Interactions to edit the segmentation can also be done with region growing.

15.4 Region growing

Region growing is a tool for doing a new segmentation and/or automatically interact with existing segmentation by only placing one inclusion and/or exclusion point. The result from the segmentation is shown in the same way as the manual interaction and can therefore remove and add to an exisiting segmentation. If no segmentation exists this tool creates a new segmentation.

15.4.1 Algorithm

The algorithm is based on a level set segmentation but the expansion speed is automatically calculated from the inclusion and/or exclusion point and only one inclusion and/or exclusion object can be segmented at a time.

15.4.2 Start the segmentation tool

The segmentation is started by placing an inclusion and/or exclusion point in the image. This is done with the tools and/or . The inclusion point should be used when a new segmentation or addition to an exisitng segmentation is the desired result. The exclusion point should be used when a part of an object shall be removed from an already exisiting segmentation. It is also advantageous to place both an inclusion and exclusion point in the image when a new segmentation is the desired result since it can give a better estimation of what intensities to include in and exclude from the segmentation. When the inclusion and/or exclusion point is placed in the image press the button Grow. To set a new inclusion and/or exclusion point use the tool once more and the old point will be removed. It is also possible to remove the inclusion and/or exclusion point with the function and/or . If more iterations is desired use the iterations slider or push the grow button once more. If more intensity expansion is desired use the expansion slider to increase or decrease it. The expansion speed can be seen in the speed image view after pressing grow.

15.5 Object manipulation

When you are pleased with an object or part of an object you can store that to a quick pick-list by the pushbutton Store. With multiple stored objects you can perform binary operations on them to merge or combine objects in other ways by using the OR, AND, NOT. You can also rename objects by the using the pushbutton Rename, or sort them in the list by the buttons Up or Down. The pushbutton Sort sorts the object by decreasing volume.

If you have many objects it is possible to store them all under different names. This is done by the function Label. This label function can also be useful to detect if two objects are joined or not. The used connectivity is

6-connectivety.

If you have one object that you want to try to split into two objects, this can be done by choosing the object in the list and using the function Split. The function erodes the object to split it at its weakest point. After the object is split into two or more parts, the algorithm reconstucts the parts so that the effects of the erosion are removed. The new objects are stored into the list.

15.6 Smoothing objects

The object is internally stored by allocating one byte per voxel. If this byte contains a value over 128, then the voxel is inside the object, otherwise the voxel is outside the object. The algorithm is binary by construction, and each voxel is given either the value 255 or 0. The contour of the exported files are created by the marching cubes algorithm, and to create a smoother result smoothing of the object representation can be performed. The slider Smooth controls the radius of a smoothing filter. The value is the number of mm to the 30% signal intensity drop of the filter. You need to experiment with the filter setting to achieve proper smoothing. For undo history and storing objects only a binary representation is used, due to memory considerations. In the Segmentation menu there is an option to create a plot of the smoothing filter.

15.7 Viewing final result

By pressing the pushbutton Plot 3D the 3D image is plotted in a separate window that can be easily rotated and zoomed. There are two checkboxes that controls the view of the isosurface ☒ Plot polygons determines whether polygons are plotted or not, ☒ Reduce patch determines whether the number of polygons should be removed by 80%.

15.8 Tools

In the Tools menu, it is possible to import segmentation from ROI's, contours, myocardium, or scar data. It is also possible to export the segmentation into

STL files that can be loaded into 3D modelling softwares, or rapid prototyping softwares. In the STL export a polygon mesh is created as a isosurface of the from the level set function. It is recommended to smooth the model prior to the STL export.

15.9 Prototype based segmentation

The prototype based segmentation is a newly developed algortihm for introducing a priori information for a specific application to the level set method used in this tool. The prototype holds both spatial information to constrain the segmentation, seed points for initialisation of the segmentation and a speed mapping function. By the use of a prototype the general segmentation can be made nearly automatic. The main idea behind the algorithm is to rather model a constrain of the segmentation, stored as a spatial map, than to model the object to be segmented. For more detailes on the algorithm see [1].

A prototype can be generated for a specific application by Medviso AB please contact us at info@medviso.com to discuss your desired segmentation applications.

To start the prototype based segmentation a couple of landmarks, defined in the protoype, need to be set by the use of the point tool . The landmarks can be set in any of the orthogonal view panels. The points shall also be named according to the information in the prototype. The specific prototype is chosen in the listbox in the panel Prototype. After the selection has been made calculations is done to align the prototype to the landmarks. When the calculations are done a light green outline is shown in the orthogonal view panels indicating the startindex of the segmentation which is used as seed points. Also the parameters radius, curvature and gradient has been set to an optimal value which was stored in the prototype. It is possible to not use the predefined startindex and/or parameters by unselecting the checkboxes ☒ startindex and ☒ parameters in the Prototype panel.

To adjust the speed image push the button Adjust speed map. The speed image for prototype based segmentation differs in several ways from the usual levelset segmentation. The image is automatically intensity adjusted which can be seen by the magnitude image being Prototype adjusted.The histogram is calculated from the adjusted magnitude image. The speed mapping mode

is Prototype shaped, and the shown function is a probabilistic fucntion stored in the prototype. Finally the Lambda slider and edit are enabled, this controls the influence of the spatial map. The spatial map is an a priori mapping stored in the prototype which constrains the segmentation. The default value of the parameter lambda is also stored in the prototype. The speed image shown is calculated from the speed mapping and by subtracting the spatial map. If any adjustments need to be done it is possible to change the Offset and Zero level but firstly try to adjust the factor Lambda since the most important part of the prototype based segmentation is the spatial map. When pressing the button [Spatial map] the spatial map is shown in a separate window. When satisfied with the speed image, press [Dismiss]. To do the segmentation press either [Go few], [Go medium] or [Go many]. If more iterations is desired it is possible to choose if the startindex from the prototype should be used as startindex should be used or not in the checkbox [☒ Startindex].

16 Save and Load Segmentation

A key feature in Segment is that all measurements and user interaction can be saved so that is possible to go back and see how the analysis was done.

Saving and loading works differently in the Clinical mode or in the research mode. In the clinical mode then Ctrl-S automatically saves to the patient database, and in the research mode you will be prompted where to store the file. Loading operations in the clinical mode opens the patient database, whereas in the research mode it opens the file loader GUI.

16.1 Save images

Segment is able to save files in three diffrent formats. One old and soon to be obsoleted that stores only the image information of one single image stack, one that stores all image stack with all segmentation into one single file and one that stores all images stacks with all segmentation into one single file that is also a valid DICOM file. The second format is the most stable and is recommended when one observer is reviewing the images, and one would like to have the opportunity to go back and check how the analysis where made. If one needs to store the file in an enviroment which only accepts DICOM images, such as a PACS, one can use the third format.

16.1.1 Save both image stacks and segmentation to one file

This function saves both the image stacks and the segmentation to one file. This is the recommended way to save the images.

16.1.2 Save both image stacks and segmentation as

Same as above, but asks for a filename.

16.1.3 Save only segmentation

To save the segmentation results (including the measurements of mass, distance measurements, viability, and volumes etc), select the function Save Segmentation under the File menu (hot key is `Ctrl-S`). Then the program asks for a filename. The file extension should always be set to `*.seg`. Note

that the segmentation file also contains scar delineations, roi's for flow analysis etc. When comparing segmentation results for different observers it is usually better to store them as separate image files with segmentation. Note this function only saves the segmentation, **not** the images. This function is kept for backwards compability and may be dropped in future versions of Segment.

16.1.4 Save as DICOM

To save as DICOM file select Special save in the File menu. Then select Save as Dicom. You will be prompted for location and filename. Note that the file is saved as a DICOM file, but essentially it is an internal file format with a DICOM wrapper. It can not be used to load and study segmentations with other DICOM compliant softwares.

16.2 Load segmentation

To load a segmentation select Load Segmentation under the File menu. The current limitations of this operation is that you should not have removed / reordered any slices compared to when you saved the file. This limitation might be removed in the future. When loading some elementary error checking is done to ensure that the loaded segmentation indeed was done on the same image stack. To disregard this safety check see importing segmentation, below.

16.3 Importing segmentation result

The difference between loading and importing segmentation is that the error checking is disabled. This means that it is possible to load a segmentation from another dataset, and overlay that on the current image stack. This could be especially useful for instance with late enhancement image where the delineation can be performed on gradient echo and SSFP cine images, and then be overlaid on a late enhancement images. See Section 12.3 on details how to translate the segmentation loaded segmentation.

16.4 Hints

Setting the data path and export path in the preferences menu (see Chapter 29) saves a lot of work when frequently loading or saving images. When

performing studies where the observer should be blinded to the identity of the patient, you can use the option to hide patient ID when loading the images. For more details see under Chapter 29.

17 Image Tools

The functions described in this chapter is in US only for off label use and for investigational use.

There are numerous possibilities to manipulate image stacks. This chapter describes the tools found under the Image tools menu in the main menu. Many of these operations are not undoable. One workaround is to before applying the intended tool, right click on the image stack thumbnail and select duplicate image stack. By doing so you do not need to reload the image stack at least.

17.1 Crop image stack

This functionality is useful to crop the images to reduce memory requirement. This functionality is not available under the image tools menu, but as a tool in the tool palette . Note that this function is not undoable.

17.1.1 Autocrop all image stacks

There is also a functionality to automatically crop all image stacks. The icon for this is found next to the crop icon.

17.2 Remove time frames

There are several suboptions to select exactly which time frames you wish to delete. Note that when you have removed time frames, you should also save the image volume since it is not possible to directly load the segmentation if it is stored as a separate `.seg` file. Note that this function is not undoable.

17.3 Remove slices

It is possible to remove all selected slices or all slices except the selected slices. When removing slices, note that you may not be able to import a segmentation to the current image stack since the number of slices will not

match. When removing slices and you want to use the data set later be sure to save the image stack. Note that this function is not undoable.

17.4 Fake in extra apical or basal slice

In some instances the most basal or the apical slice may be missing due to improper scan planning. This should be avoided and be reported back to the scanning operator. However, if it still occurs the image set might be possible to rescue the image stack with this operation. It inserts a copy of the basal or apical slice and the segmentation. The reason that this might work is that it might be possible to copy the delineation of the basal slice in end diastole to the second most basal slice in end systole.

17.5 Manipulate light/contrast

Once loading image data from DICOM files Segment internally converts the image data to the range [0..1]. The conversion factors are stored and the original pixel intensities can thus always be recovered.

17.5.1 Permanently apply light setting

When adjusting contrast and brightness the changes only affect the on screen appearance. With this option the current light setting is permanently applied to the image stack. This will then have impact on subsequent image quantification. Note that this functionality is not undoable.

17.5.2 Normalize image data

When loading image stacks from `.mat` files this check is not performed. Normalize image data will do this process. This process is currently not undoable even though all the required data is stored.

17.5.3 Invert colors

Invert colors remaps all pixels with the equation $s_{new} = 1 - s_{old}$, where s denotes pixel intensity. This functionality is undoable by repeating the operation.

17.5.4 Precompensation

This functionality might be useful for gradient echo MR images to minimize inflow artefacts. This option scales each time frame such as the mean image intensity is constant over time. Note that this function is not undoable.

17.5.5 View intensity mapping

Brightness and contrast settings are implemented so that the pixel intensity is remaped before being rendered. Currently this remaping function is a cropped linear function, but will be extended to a sigmoid function in future versions of Segment. This functionality plots the current intensity mapping.

17.5.6 View true image intensity

The function displays the current slice and time frame, and a color scale coupled to the original pixel values in the DICOM file.

17.6 Set colormap for current image stack

This function sets the used colormap for the selected image stack. Supported colormaps are shown in Figure 24.

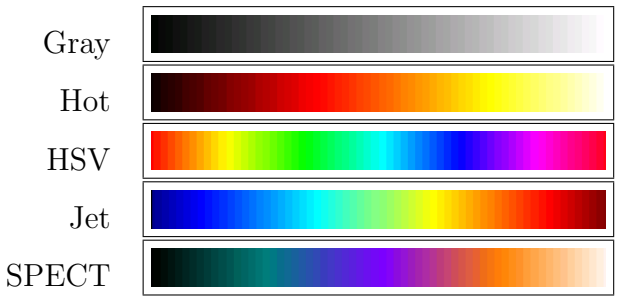


Figure 24: Colormaps.

17.7 Flip/Rotate image stack

By using this function it is possible to swap the direction of one axis. For instance if want to flip an image stack upside-down (apex/base) use Flip z.

Flip x corresponds to what one usually would call y-axis, and for a short axis image stack this would usually be frontal/dorsal, and Flip y corresponds to left/right. Note that to preserve a right hand coordinate system it is not possible to flip in one image direction alone. Therefore, a flip in x directions also flips in the z direction. The simple flip's above is possible to do when there is an existing segmentation. If you require to make rotations (flip between two axis) you must not have an existing segmentation. Flip x&y transposes the image, Flip x&z switch between basal/apical to up/down direction, and Flip z&t change between time frames and slices. The later option is very useful when loading non standard images. This option does not update coordinate axes so this might be dangerous to use if combining with non flipped image stacks. If you need to rotate image volume and maintain correct voxel dimensions, please use the multiplanar reconstruction (MPR) functionality described in Chapter 30. Note that currently the option to rotate 90 degrees right is not working properly.

17.8 Resample image stack

There are different methods to resample the original image stack.

17.8.1 Reformat multiplanar reconstruction)

This option invokes the multiple planar reconstruction tool described in Chapter 30.

17.8.2 Upsample/downsample image

By using this option it is possible to upsample or downsample the image stack. Note that resampling is only done in the in-plane direction. When downsample an appropriate anti-alias filter is applied. The used interpolation algorithm is bicubic interpolation. This functionality is not undoable.

17.8.3 Upsample/downsample slices

The number of slices can be upsample of downsampled. This functionality is not undoable.

17.9 Add noise

By using this functionality it is possible to add noise Gaussian white noise to the current image stack. The amount of noise is regulated by the std of the noise.

17.10 Calculate temporal mean image

This function creates a new image stack that is the temporal mean of the current image stack.

17.11 Set current frame as first frame

This function shifts the time series (cyclic shift) such as the current time frame becomes the first time frame in the time series. Note that it only applies to selected slices.

17.12 View K-space

This menu option shows the k-space for the current frame and slice.

17.13 Set image description

By using this menu option the image type, image view plane and imaging technique is displayed and a menu is shown where new image descriptions can be selected. Image type and image view plane is used by Segment to find what image stacks to take measurements from. This applies to the utility to summarize multiple `.mat` files and the report sheet generator. Imaging technique is used to find segmentation parameters and are therefore critical for a good automated segmentation. For further details, see Section 12.3.

17.14 View Image details

This function copies the most important image details to the clipboard. It is the same as the icon .

17.15 View and adjust image details

By using this menu option it is possible to adjust image details. Parameters that can be adjusted are Slice thickness, Slice gap, Resolution in x direction, Resolution in y direction, and time increment.

17.16 View and adjust patient details

This menu option starts a graphical user interface where it is possibly to view/adjust: Patient Name, ID, birth date, acquisition date, age, height, weight, sex. The pushputton Apply to all applies the changes to all image stacks that are loaded to memory. By entering height and weight, BSA is automatically calculated.

17.17 Remove subject identity

By using this menu option all patient data are removed from all image stacks. This is useful when sending data to a different center or for bug report purposes. This function is not undoable. Removed items are patient name, id, birth date, acquisition date, filename, and original filename.

17.18 Calculating image histogram

Image histogram can be calculated by using tools found under the ROI-menu. For further details, see Section 18.6.

18 Region of Interest Analysis

The region of interest (ROI) functionality can be used for a wide range of possibilities. To select the ROI mode you can use the hot key `Shift-F`.

You can label and color each ROI individually. For flow measurements each ROI can also be assigned with a sign that will be multiplied with the velocities inside the ROI. The default sign is positive. The following names of ROI's are reserved for various purposes:

- Remote ROI (used to implement 2SD from remote as described by [3]).
- Scar region ROI (used to implement 2SD from remote as described by [3]).
- Static tissue (used for concomitant field correction, described in Chapter 23).
- Aortic ascending flow
- Aortic descending flow
- Pulmonary artery
- Vena cava inf
- Vena cava sup
- Vena pulmonalis inf
- Vena pulmonalis sup
- Vena pulmonalis dex
- Vena pulmonalis sin
- Sinus coronarius
- Lung
- Heart

18.1 Creating ROI's

There are several possibilities to add ROI's. Perhaps the most intuitive method is to draw the ROI by using the . The ROI will be given the same

name, and color as the latest modified/drawn ROI. This is very useful if you would like to draw several ROI's of the same kind. Start by drawing the first ROI, name and color it. Thereafter you can continue to draw the remaining ROI's.

It is also possible to add fix sized ROI's by using the Add fix size ROI under the ROI menu. This will add a fix size ROI and you will be prompted to enter the diameter. This function applies to the current slice. Another approach is to add ROI's in the myocardium between the endocardium and epicardium. This is done by using the function Add ROI's in sector (selected slices). You will be prompted for center angle, width in degrees, percent from the wall. Zero center angle corresponds to three o clock and counting counter clock-wise. This function only adds sectors in selected slices. An example of automatic ROI placement is shown in Figure 25.

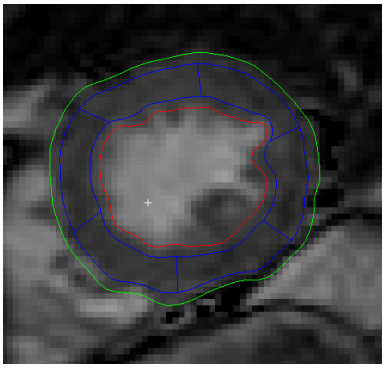


Figure 25: Automatic placement of ROI's inside the myocardium.

Another possibility to create ROI's is to convert the endocardial, epicardial or scar surface to a ROI. This is done by the option Copy endocardium to a ROI, Copy epicardium to a ROI or copy scar to a ROI. This only includes the selected slices.

18.2 Modifying and deleting ROI's

By right clicking on a ROI a pop-up menu appears where it is possible to:

- Delete ROI
- Set ROI label (change the name/function of the ROI).
- Set ROI color (change the color of the ROI).
- Copy ROI upwards
- Copy ROI downwards
- Copy ROI outline to all timeframes
- Refine ROI (for flow purposes, see Chapter 23).
- Switch ROI sign (useful for flow analysis).

18.3 Translating and scaling ROI's

ROI's are translated with the icon and scaled with . Point on ROI contour and drag while mouse button kept down to adjust to correct position/size.

18.4 Deleting ROI's

Under the ROI menu it is also possible to Delete ROI, Delete ROI's Using Template, and Clear All ROI's. The first menu option deletes the current (last drawn or modified ROI). The second menu option deletes ROI's with a name matching a specified template. A menu of possible ROI's that can be deleted are shown.

18.5 ROI analysis

It is possible to plot and export the following parameters over time:

- Mean signal intensity
- Standard deviation of signal intensity
- ROI area
- ROI area based on pixels
- Minimal signal intensity
- Maximal signal intensity

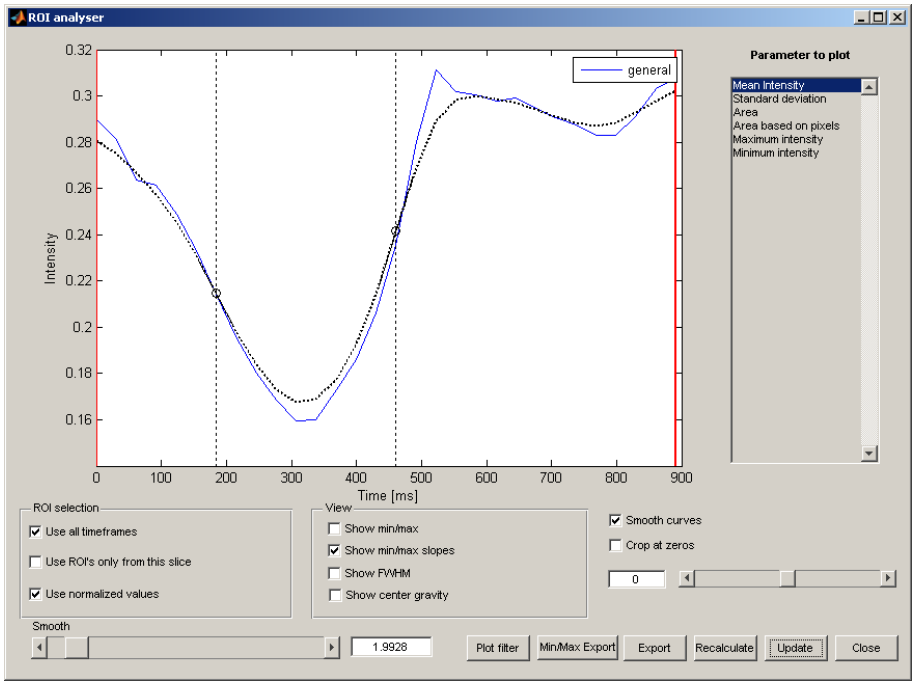


Figure 26: Graphical user interface for ROI analysis.

An example of the user interface is shown in Figure 26. In the ROI-selection panel the ROI's to plot can be selected. If the checkbox ☒ Use ROI's only from this slice is selected, then only ROI's in the current slice are shown. If the checkbox Use normalized values is selected the the values are shown in the `Segment's` own internal normalized representation. Otherwise the values are recalculated back to the pixel values in the DICOM files. In the View panel it is possible to select to plot min/max values, min/max slopes, or Full-Width-Half-Maximum (FWHM). If the checkbox ☒ Smooth curves is selected, then the curves are smoothed before slopes, and min/max values are calculated. The smoothing is applied is a Gaussian smoothing kernel. The smoothing parameter σ is adjustable with the slider, and the edit box. By using the Plot filter button it is possible to plot the filter in the temporal domain. Currently the filter is applied directly to the ROI curve. Finally, the Export button exports all parameters to the clipboard. The Max/Min Export button exports the values and timing of min/max, min/max slopes, and FWHM. Note that that when changing plotting options the plot is not updated until you click Update.

18.6 ROI histogram

This function plots the histogram of ROI(s). When initiated the program asks for a selection criteria on what ROI's to include. If no ROI's are present then the histogram for the whole image (current slice and time frame) is displayed. The most common percentiles are also calculated and exported to clipboard. An example is shown in Figure 27.

18.7 Multiple threshold analysis

This function calculates the number of pixels inside the ROI's above the selected threshold. Before starting the program prompts for start threshold, end threshold and number of levels. All curves are plotted at the same level. The offset of each curve is displayed. All numeric data are copied to clipboard. There is also a visual mode where the pixels above a certain threshold are color-coded. An example of the visual analysis is shown in Figure 28. You are also prompted whether to use the internal normalized image pixel values or the original data from the file. The non-normalized range can be found by plotting the image intensity mapping (found under Image tools). By

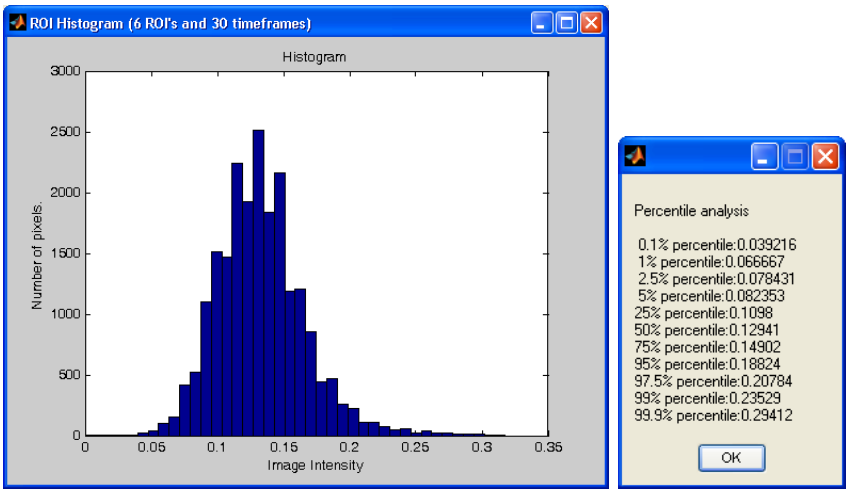


Figure 27: Example of ROI histogram.

selecting Multiple threshold analysis - numeric the same analysis is performed for each time frame and numeric values are exported to the clipboard.

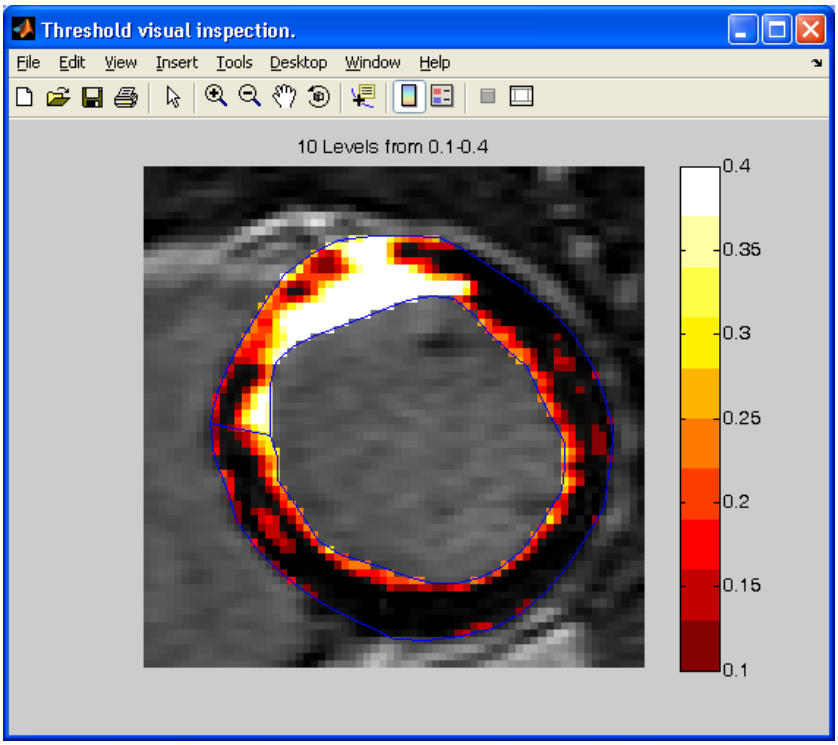


Figure 28: Example of multiple threshold analysis.

19 Measurements and Annotations

The whole software package Segment is designed for quantitative analysis and subsequently there are a rich variety of measurement tools available.

19.1 Length measurements

There are two possibilities to make length measurements. The easiest method is to use the measurement tool . To place a linear measurement, left click with the mouse, hold mouse button down and drag mouse to the desired location. Alternatively, or to place a measurement consisting of several line segments, hold down the `Shift` key while clicking to place end-points. Finish by clicking with `Shift` released. You are then asked to annotate and give the measurement a label. It is possible to refine the position of the measurement by click one of its end-points and drag that to the desired position. The measurement with its annotation is shown in Figure 29. Under the Annotations menu it is possible to clear or export all measurements to the clipboard. Measurements of ventricular wall thickness is best performed by using the tools for region wall motion analysis described in Chapter 26.

Another method to get distances (or timing intervals) by adding annotation points at different points in space and time. Annotation points are added with the icon and export the coordinates and time points of the annotation points to Excel or another spread sheet program and there calculate the distance. Annotation points is also useful for marking anatomical landmarks etc. For further details, see Section 19.7.

19.2 Timing

By using the M-mode viewing mode it is possible to make measurements of both timing and distances. This is illustrated in Figure **??**, on page **??**.

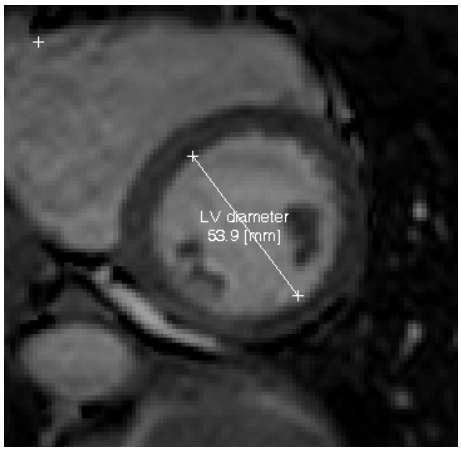


Figure 29: Example of a measurement of the left ventricle diameter.

19.3 Volumes

Volume of the left ventricle is displayed and updated as soon as you have delineated some slices. If the volume was calculated from segmentation in longaxis images, this is indicated in a line of text above. Volumes of ROIs can be derived by using the numeric multiple threshold analysis described in Section 18.7. On possible mistake when doing manual delineation of the left ventricle in only diastole and systole is the failure to indicate what time frames that are end-diastole and systole respectively. This will cause `Segment` not to show any volumes. Selecting diastole and systole can be done by interactively dragging ED and ES in the volume graph or using the Autodetect End systole and End diastole under the Edit menu.

19.4 Area

Area of ROI's can be derived by using the region of interest analysis tool in Chapter 18. In certain cases area can also be derived by dividing volumes by the slice thickness. The area of the ROI's is shown for each ROI in the one slice view. In the near future a general area tool will also be added to Segment.

19.5 Flow and volumes

Measurements of flows and volumes are covered in Chapter 23.

19.6 Signal intensity

Signal intensity can be measured by using the region of interest analysis tools described in Chapter 18.

19.7 Annotation and anatomical landmarks

Annotations are added with the ABC icon or under the Annotation menu. The points can either be stationary or time resolved (i.e have different positions in different time frames). The stationary points are marked with a bold font. To make a pointtimeresolved right click on it and select Make point timeresolved from the pop-up menu. Note that this operation is undoable. It is possible to Clear All Annotation Points, Clear Annotation Points Using Template, Rename Annotations Using Template, and Export All Annotation Points. When deleting or renaming using a template you are prompted for a template. The template must be an exact match since no wildcards are allowed.

To propagate the location of a time resolved point, press `Ctrl-F`. Note that you need to have the annotation tool ABC active when doing this.

20 Utilities

The functions described in this chapter is in US only for off label use and for investigational use.

The differentiation between a utility and a function/feature is that the utility does not necessary apply to an image stack. Currently there are five utilities available.

20.1 Anonymize DICOM files (Recursively)

This function ask for a folder of DICOM files and replaces the patient name with a new name for all the DICOM files. Caution since it overwrites the existing DICOM files, and it is recommended to backup these files prior to running this function. The function change PatientName and removes patientID, DateofBirth, OtherPatientIDs, EthinicGroup, Occupation, AdditionalPatientHistory, PatientComments, InstitutionAddress, and InstitutionName.

20.2 Anonymize `.mat` files (Recursively)

This function takes a folder of .mat files and anonymize the files and change the patient name to the filename of the .mat file. This function is particularly useful when anonymizing a complete research study.

20.3 Clear segmentation from multiple `.mat` files

This utility is useful when one want to clear the segmentation from multiple .mat files at once. One particular example when it is useful is when a second observer should reanalyse all files. In such cases copy all files, rename them and run this function.

20.4 Sort Folder of DICOM files

This utility is useful when you a have a large collection of DICOM files that are in a strange order. This is often the case from certain Siemens scanners. The program will sort them up in folders that are arranged as

patientname+patientid, studydate+stydyid, and series number. Each folder will contain sorted files according to instance number and trigger time.

The graphical user interface is shown in Figure 30.

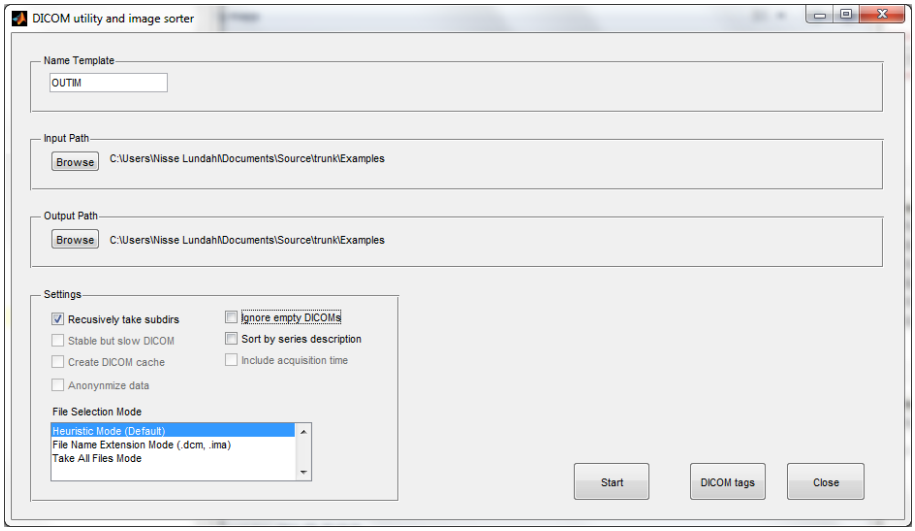


Figure 30: Graphical user interface for the DICOM sorter.

Start by selecting input and output folders/path/directories. If the checkbox ☒ Recursively take sub dirs is selected then the program will take all files below the selected input directory including its subdirectories. The input/output folders should preferably not overlap. Each file will be named according to the name template followed with a 5 digit number. The function DICOM tags asks for a filename and displays all DICOM tags in that particular file. The checkbox ☒ Stable but slow DICOM controls what DICOM interpreter is used in the sorting operation.

If you select the checkbox ☒ Create DICOM cache then the program will create cache files that are used when loading DICOM data into Segment. This will significantly speed up loading and is therefore recommended. For more details of caching of DICOM files, see Chapter 9.
The checkbox ☒ Ignore empty DICOMs allows the user to leave out files where the AcquisitionDate tag is either empty or broken, which is an indication of

an empty file. If a series is broken up into parts with separate series numbers, ☒ Sort by series description sorts all files with the same series description into the same directory. If this is selected, ☒ Include acquisition time can be used to include acquisition time in filenames, thus making the time order of files in the series directory easy to follow.

20.5 Copy and Sort Images from CD to Data Folder

This function is ideal to use when you have images on a CD (structured or not) that you want to copy to your harddrive and subsequent analyze. This function assumes that you have set the location of your CD drive in the preferences (see Chapter 29). This function sorts and name the files in the same manner as the sorting utility. DICOM cache and thumbnails are also created.

20.6 Create DICOM cache for folders recursively

This function ask for a folder and creates DICOM cache files for all subdirectories. This functionality is highly useful when you have copied large sets of DICOM files to your local harddrive that you need to load into Segment. It takes a long time to run so a good idea is to start this function over lunch. Once this is done loading of your DICOM files will go much faster.

20.7 Create thumbnails preview recursively

Analog to creating of DICOM cache files but creates thumbnail preview for all subdirectories. Depending on the number of subfolders this function may also take quite long time to run.

20.8 Find patient details in .mat files

This utlity allows to scan your entire harddrive (or network drive) for patient details in .mat files. Output is a list of all patients occuring in the directory tree. This feature is useful when you want to ensure that you have not stored any sensitive information on your local computer/laptop for instance. The output is an Excel file where each row .mat file with patient information.

20.9 Find patient details in DICOM files

Analog to the above function, but instead looks in all your DICOM files. The following heuristics is used to classify a file as DICOM or not:

- Files that ends with `.dcm`.
- Files that only contains digits and no extension.
- Files with name that contains more than 7 dots and the two first letters corresponds DICOM identification of an imaging modality.

The output of this function is an Excel file where each line is one unique patient identity and the number of files in which the patient name was found. Note that to be completly certain about the are no DICOM files with the patient details you need to count the number of files that are deleted / anonymized for each patient or simply run the function twice.

20.10 Export from multiple `.mat` files

This function summarize multiple `.mat` files into one summary. This is very useful for research studies. For instance by placing `.mat` files, one for each patient in one folder. It is possible to summarize all patient data into one Excel sheet. Note that each `.mat` file can contain several image stacks. The program automatically determines what image stack is for instance short-axis slices, and what image stack is viability images. If this automatic image stack detection fails it may be necessary to load the image stacks and select correct image type. For further details see Section 17.13. Currently the following data is outputed for each files; File name, Patient name, Patient ID, Age, Length, Weight, Sex, BSA, Heart rate, R-R interval, LVM in ml, LVM in g, EDV, ESV, EF, LVM from viability images, Scar percentage, Scar in ml measured on viability images. Furthermore, for each ROI in the image stack the name of the ROI and the total volume is reported. When EDV, and ES is not exported see Section 19.3 for hints.

20.11 Export Information from multiple `.mat` files

This function exports imaging information from multiple `.mat` files. Example on exported information is:

- `ImageType`

- Image size
- Resolution
- Slice thickness and slice gap
- Time increment between
- Information whether the file contains infarct sizing, flow information, segmentation

21 Viability Analysis

The functions described in this chapter is in US only for off label use and for investigational use.
The viability tools can be found under the MR menu in Segment. The method used for automated delineation of infarct is described in [4]. It uses a new paradigm in analyzing delayed contrast enhancement MRI. Instead of treating each pixel as dichotomously infarcted or not infarcted pixels are weighted with their signal intensity.

The new method delineates a larger area than the previous method [5]. It should be noted that even though it delineates a larger area, this should not be compared to manual delineation, since the darker pixels are given a lower weight. As a graphical illustration of this a pink line is also shown in the weighted mode. An example of this is illustraded in Figure 31. This line graphically represent the corresponding non weighted area. Please note that this line is only provided for visual feed-back and should not be used for any quantification purposes. The weighted scar delineation method is extensively validated in animals, computer phantoms and 40 patients on images acquired both on Siemens and Philips MRI scanners.

The first step to do viability analysis of delayed enhancement MRI (DE-MRI) images is to delineate both endo- and epicardium. This can be done either manually or by a semiautomated method. In many cases however, it may be faster to manually draw the endo- and epicardial contours. Then select Auto Delineate Viability (Weighted method) to delineate infarct. The automated delineated infarct is now shown with a yellow contour. After the delineation you can select the mode of operation. The default mode to use is the weighted automatic scar delineation (see below for details).

In the Viability menu you can select mode of operation, reset all scar delineation, reset user corrections, control visibility and automatic parameters. It is possible to add infarct regions by using the pen tool

and remove infarcts with the rubber tool regardless of the mode of scar delineation. The tool removes the manual corrections made with the

or . By default manually added scar regions shows up in green and manually deleted

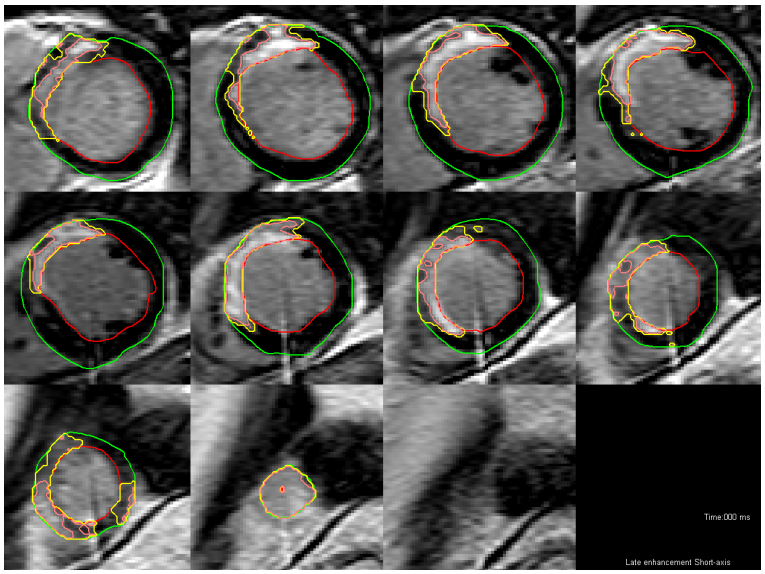


Figure 31: Example of scar delineation in the weighted mode. The yellow line denotes the complete affected area, and the pink line a graphical representation of the corresponding weighted area.

areas in blue. The tool is used to manually draw regions of microvascular obstruction. Microvascular obstruction is indicated in red. User interaction (and microvascular obstruction) can be showed/hided by clicking the key o. Note when using the weighted method, regions with microvascular obstruction needs to be manually drawn if not automatically detected, since otherwise they are weighted incorrectly. It is also possible to remove regions with microvascular obstruction with the toggable menu option Remove microvascular obstruction. Apex post processing is a technique described in [5] to handle case where the complete slice is infarcted. This functionality should normally be enabled.

The following modes of scar delineations is available:

- None. No viability, this will remove viability delineations.
- Manual mode. Manual drawing of hyper enhanced regions
- Automated Method (Weighted - default). Automatic scar delineation as described in [4].
- Automated Method (SCJ method). Automatic scar delineation as described in [5].
- FWHM. Automatic scar delineation using a full width at half maximum method, as described in [6].
- SD from remote. Implementation of taking two 2-SD from remote myocardium as proposed by Kim *et. al* [7]. You need to place ROI's in the myocardium and label them ase 'remote'.
- K-means. Using the k-means algorithm, with two normal distributed classes (infarct and non infarct). Original algorithm described by [8].
- EM algorithm. Using the EM algorithm, with two normal distributed classes (infarct and non infarct) as described by [**?**].

Each of the different methods are further described below.

21.1 Automatic mode weighted, SCJ or FWHM

The automatic mode is the default mode. In cases where it fails make necessary manual corrections by using the tools and respectively. Note that including extraneous black regions in the weighted method only marginally

changes the result, since the infarct is weighted with pixel intensity. In the weighted method it may be necessary to manually mark regions of microvascular obstruction to get these regions weighted correctly.

21.2 Manual mode

In this manual mode the infarct area is not automatically updated and the only way to change the delineation is by doing manual interactions. If you want to start from scratch to manually draw your infarct regions, then first select Clear all scar data. This option also resets the viability mode to Automatic mode so you need to choose Manual mode before starting to draw the infarct regions.

21.3 SD from remote

It is possible to do scar delineation as proposed by Kim *et. al* where the infarct is determined as pixels with an image intensity that is higher than the mean plus two standard deviations from the mean in a non infarcted remote region. In the original method by Kim et al when one read the paper carefully they used two types of ROI's, both remote ROI's and also a scar region ROI in which the thresholding was applied. Therefore, the same approach is also applied in Segment.

To draw remote region use the ROI drawing tool or Add ROI's in sector under the ROI menu. The latter option adds ROI's in a sector in selected slices with a position specified as an angle, the width as and angle and finally the distance from the endo- and epicardium as percentage of the wall thickness. This option automatically flags the ROI's to be remote regions, but if you use the ROI drawing tool you need to manually flag that by right clicking on the ROI and select Select ROI label on the pop-up menu. When drawing a subsequent ROI the label of the ROI is copied from the last modified ROI so you only need to first draw one ROI, then label it and draw all remaining ROI's. If you do not draw a remote region in the threshold for that slice is then intra/extrapolated from adjacent slices. Using the default viability options this approach will only set a threshold to the level set algorithm based on the drawn ROI's.
To draw the scar region ROI's (Scar region ROI) use the same approach as described above. It is often advantagoues to first draw all the remote ROI's

and then the scar ROI's since you do not need to alternate with labeling the ROI's.

In a final step to use the method of standard deviations from remote, you need to set the parameter Beta to zero. To change the standard deviations from remote, see under Technical details below.

21.4 EM algorithm

This automatic mode is developed for ex-vivo studies. In cases where it fails make necessary manual corrections by using the tools and respectively. It may be necessary to manually mark regions of microvascular obstruction to get these regions delineated. The weighting mode should not be turned on for high resolution ex-vivo CMR images.

21.5 Technical details

It is possible to control the parameter Beta, Min volume, Standard deviation from remote. The parameter Beta controls the smoothness 'curvature' forces on the level set surface and in practice it controls the smoothness of the result. The parameter Min volume controls the minimum size allowed for an infarct in ml. The parameter Standard deviations from remote controls how many standard deviations from remote that should be taken when calculating a slice based threshold. The default for the automatic mode is 1.8 for the weighted algorithm, and 2.4 for the SCJ method. Generally this should only be changed when using the mode SD from remote. These parameters are further described in [5, 4].

21.6 Grayzone Analysis

Two different methods for Gray Zone analysis is provided in Segment. The two methods are the Weighted method and the ROI method.

21.6.1 Gray Zone analysis by weighted method

The menu item Gray Zone Analysis (Weighted Method - Default) enables the user to divide the scar area into core and grayzone based on the scar segmentation. The result is displayed in the image view as colored overlays of

dark red (core) and dark yellow (grayzone) pixels. The quntitative core and grayzone values are presented in a message box.

21.6.2 Gray Zone analysis by ROI method

The menu item Gray Zone Analysis (ROI Method) enables the user to divide the scar area into core and grayzone based on ROI segmentations and a user selected threshold. The result is displayed in the image view as colored overlays of dark red (core) and dark yellow (grayzone) pixels. The Grayzone Analysis GUI displays a histogram of the pixel intensities of the currently segmented scar volume. By dragging the red bar, the user can change the threshold for what identifies as grayzone (intensity values lower than that of the bar) and core (the remainder). The user can also change the threshold for scar segmentation, given as number of standard deviations from remote value, by clicking the Increase or Decrease buttons. After changing either of these thresholds, the values are recalculated by clicking the Recalculate button. The sizes of the core and grayzone volumes are calculated based on pixel volume and displayed in the GUI, and can be exported along with the threshold values by clicking the Export button.

22 Myocardium at Risk Analysis

The functions described in this chapter is in US only for off label use and for investigational use.

The maR tools can be found under the MR menu in Segment. The method used for automated delineation of MaR is described by Sjogren et al [9]. It uses an Expectation Maximization algorithm to calculate a probability of MaR based on intensity instead of using a threshold and models of the perfusion territories are used as a priori information to constrain the segmentation.

The first step to do MaR analysis of T2-weighted MRI (T2w-MRI) images is to delineate both endo- and epicardium. This can be done either manually or by a semiautomated method. In many cases however, it may be faster to manually draw the endo- and epicardial contours. Then select Auto Detect MaR to delineate MaR. In the graphical user interface choose the culprit artery in the list box and rotate the yellow line to indicate the inferior insertion point of the right ventricle and press OK. The automated delineation of MaR is now shown with a white contour.

It is possible to add infarct regions by using the pen tool and remove infarcts with the rubber tool . The tool removes the manual corrections made with the or . By default manually added mar regions shows up in green and manually deleted areas in blue.

23 Flow Analysis

This functionality may depend on your MRI scanner. Currently it has been tested using Siemens, Philips and GE scanners.

When flow image stacks are displayed, the screen should now similar to what is shown in Figure 32. On the left image panel the magnitude image is shown and on the right image panel the phase image is shown. When a flow image stack is selected a white frame around both the magnitude image and phase image is drawn in the thumbnail preview area. This helps to keep track of which phase images belongs to which magnitude images.

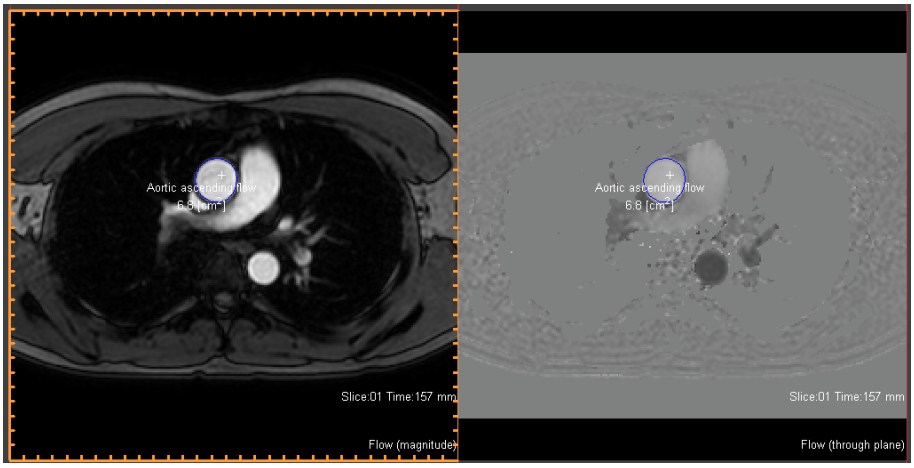


Figure 32: Example of main GUI in flow mode.

23.1 Automatic segmentation of flow ROI's

The suggested method is to select the ROI tool . Then draw a ruff outline of the vessel contour. Thereafter start the automated vessel tracking and refine. This is done by pressing `Ctrl-T`.

Another method to automatically segment a vessel is to drag the center cursor (white +) to the approximate center of the desired vessel and press `Ctrl-G`,

or Auto delineate a vessel under the Segmentation→ROI and Flow Tools menu. The vessel is automatically delineated and you are asked for an appropriate label. Deleting, renaming, recoloring the region of interest is described in Chapter 18. If you are not satisfied with the ROI there are two methods that can be applied.

23.1.1 Refine

Refine operation operates on the current time frame or all time frames depending on the checkbox ☒ Single frame mode. Short key for the refine function is `Ctrl-R`. You need to have the ROI pen active when using the hot key. Refine on all time frames is particularly useful if the vessel is fairly round and not to close to other surrounding tissue.

23.1.2 Refine and propagate

Start at the first time frame of the time series. If pleased with the result simply use the right arrow key on the keyboard to proceed to next time frame. When you find a time frame where you are not pleased with the segmentation use the ROI pen to adjust the contour or use the refine option Ctrl-R with the checkbox ☒ Single frame mode enabled. Continue by propagating the contour by pressing `Ctrl-F`.

23.1.3 Shrink flow ROI

If the RIO is outside the vessel then it might be advantageous to shrink the ROI followed by one ore more refine operations. Shrink flow ROI is found under the Segmentation menu and the submenu ROI and Flow tools.

23.2 Plotting the result of the flow analysis

The flow plotting utility is started by using the icon or by using the function Plot flow curves under the Flow menu. An example of the graphical user interface is shown in Figure 33.

In the upper right area of the GUI you can select which parameter to plot. The volumes presented in Volume panel of the GUI represents flow integrated between the two vertical red bars. These bar can interactively be moved with the mouse to control the range of the integration. Forward volume is the volume of the flow integrated only over the time frames where the

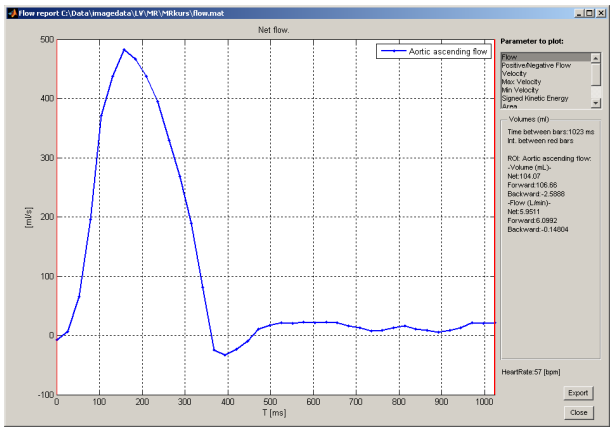


Figure 33: Example of flow plotting GUI. Plotting parameter can be selected in the upper right corner of the GUI. The flow integration is performed between the two red bars.

net flow is positive (forward). Backward volume is the volume of the flow integrated only over the time frames where the net flow is negative (backward). This should be contrasted to the flow parameter Forward/Backward that plots simultaneously the flow that goes forward and backward of the region of interest. Note that there can be significant backward flow in one time frame even though the net flow is forward in that very time frame. An example on the latter is shown in Figure 34. The sum of the two curves is the same as the net flow that is shown in Figure 33.

It is also possible to plot the Velocity over time, and this is shown in Figure 35. The 'error bars' denote the standard deviation of all pixels in the ROI of that particular time frame.

Another possibility is to plot the max or min velocity in the ROI over time. It is also possible to plot the radius and diameter over time. The radius are calculated as; what diameter need a circular vessel have to have the same area as the area of the ROI. The option Signed Kinetic Energy calculates the kinetic energy in the blood assuming standard density of the blood.

The final possibility is to plot a 3D profile of the velocity distribution of the vessel. This can be plotted for all time frames at once or only a single time

frame that later can be stepped forward/backward in time. An example of the 3D plot is shown in Figure 36.

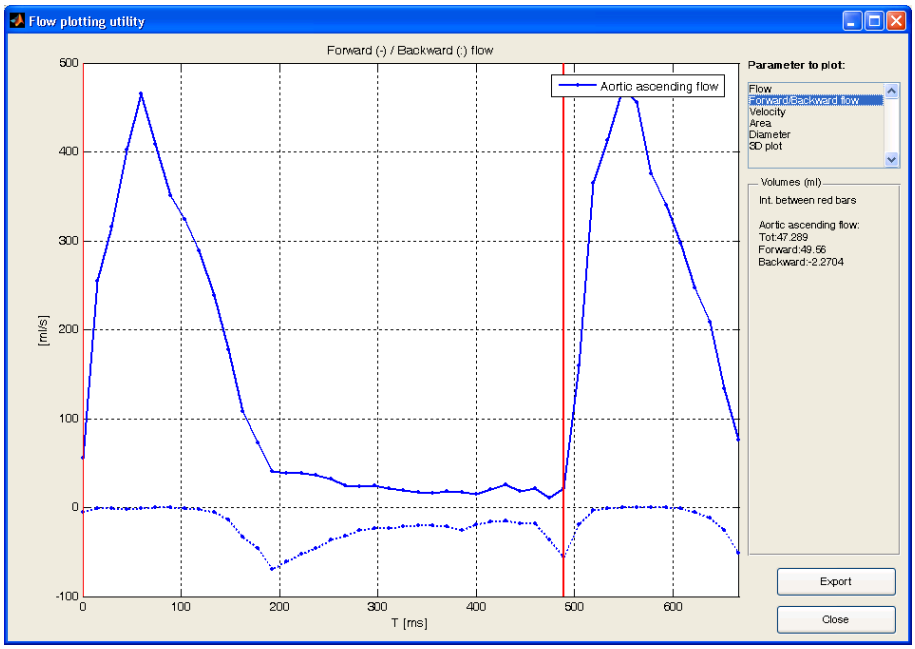


Figure 34: Example of plotting of backwards and forward flow simultaneously. The sum of the two curves will be the net flow showed in Figure 33.

23.3 Compensating for eddy current effects

To get accurate flow measurements it is important to compensate for concomitant field effects such as eddy currents, and Maxwell effects. Ideally Maxwell effects should be compensated for directly on the MRI scanner since it can be analytically calculated. Consult your MRI vendor for details about how this is implemented in your scanner. Note that when compensating for eddy current effects the image stack should not be cropped upon loading, since the algorithm need phase information of static tissue in the chest wall to function properly.

The graphical user interface for compensating for eddy current effects is shown in Figure 37.

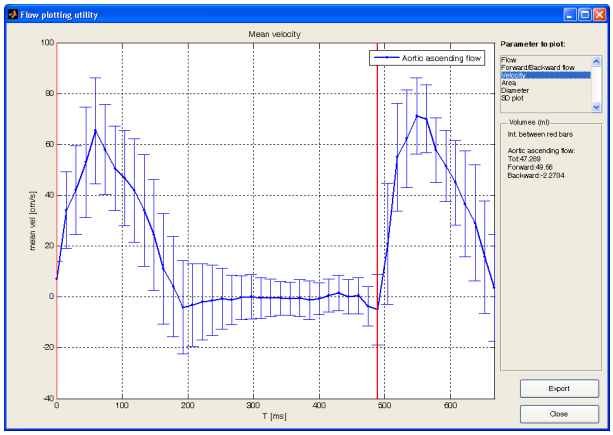


Figure 35: Example of plotting of velocity over time. The 'error' bars shown the standard deviation of the pixels within the ROI over time.

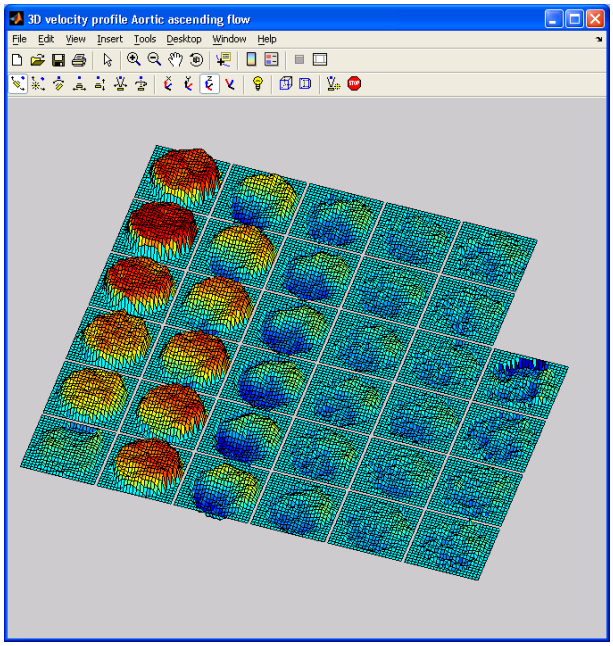


Figure 36: Example of plotting of a 3D profile of the velocity distribution.

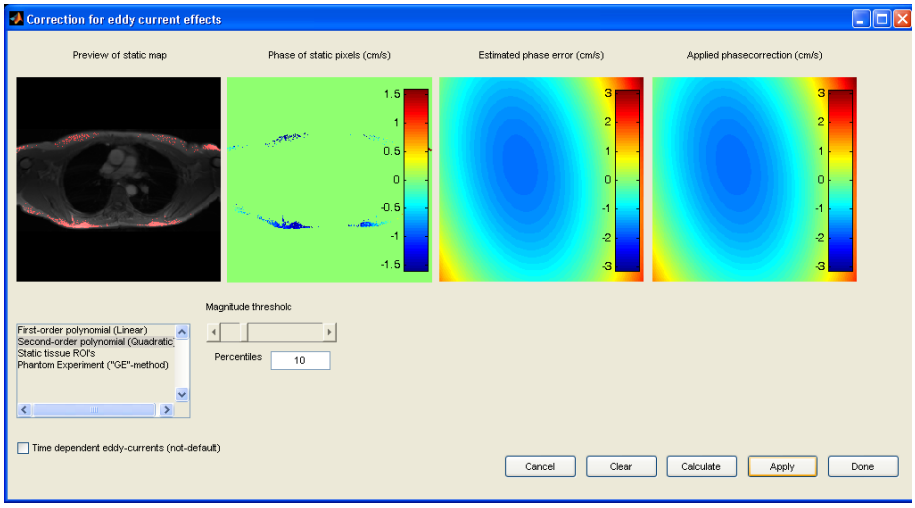


Figure 37: Example graphical user interface for compensating of concomitant field effects. In the left the identified static tissue is the displayed, and in the middle panel the corresponding phase for these pixels is shown, and in the right panel the resulting phase correction is shown.

You can select model order, and clear the phase correction. When you are pleased with the phase correction press Apply to proceed. The function automatically finds stationary parts in the image by selecting a percentage of the pixels whose standard deviation of the phase over time is smallest. The fraction of pixels taken can be controlled by the edit box Percentile. The image is divided into four quadrants and the algorithm to find stationary pixels is applied to each quadrant separately. This is done to ensure that there are about the same number of pixels from each quadrant. Pixels taken as stationary tissue are shown as red dots in the magnitude image. The Magnitude slider controls what magnitude the pixels need to have before being labeled as stationary. By selecting the mode of operation as Static tissue ROI then ROI's that are labeled Static tissue are taken as stationary areas. This is particularly useful when doing phantom experiments, since the automated identification of static areas fails in cases with stationary flow. The mode of operation `Phantom Experiment (GE-method)` automatically finds a flow image stacks that have the same scanning parameters this useful

when a static tissue have been scanned in the same position as the patient as recommended by GE for eddy current compensation. For usage, see paper by Alex Chernobelsky *et al.* [10].

23.4 Phase unwrapping

In cases were the velocity in the blood is higher than the VENC the velocities can wrap around. Under certain conditions these phase wraps can be uncovered and phase unwrapping can be performed to retrieve the correct velocities. The graphical user interface for the phase unwrapping tool is shown in Figure 38.

The checkbox ☒ Show ROI pixels shows the pixels that are used in the ROI in a red color. This is useful when one want to know exactly what pixels are included in the ROI. The checkbox ☒ Use magnitude mask is used when one want to limit the automated phase unwrapping only in pixels that have a magnitude over a certain threshold.

23.4.1 Automated unwrapping

The automated phase unwrapping algorithm works on a pixel by pixel basis and operates along the temporal dimension. It looks for pixels where the phase appears to have wrapped once up and once down. Therefore the algorithm will fail for a biphasic velocity profile if phase wrapping occurs at both phases. Furthermore, it only considers single wrap arounds (i.e the phase is assumed to have wrapped once).

23.4.2 Manual unwrapping

There are four tools available, . The tool is used to pan the images. The second tool wraps the pixel up at left mouse button clicks. The third tool wraps the pixel down at left mouse button clicks. The fourth tool is used to plot the phase of the current pixel over time. This is mainly useful for debugging purposes. It is possible to zoom the image by usage of the zoom icons . Undo last operation is done by pressing `Ctrl-Z` or the icon .

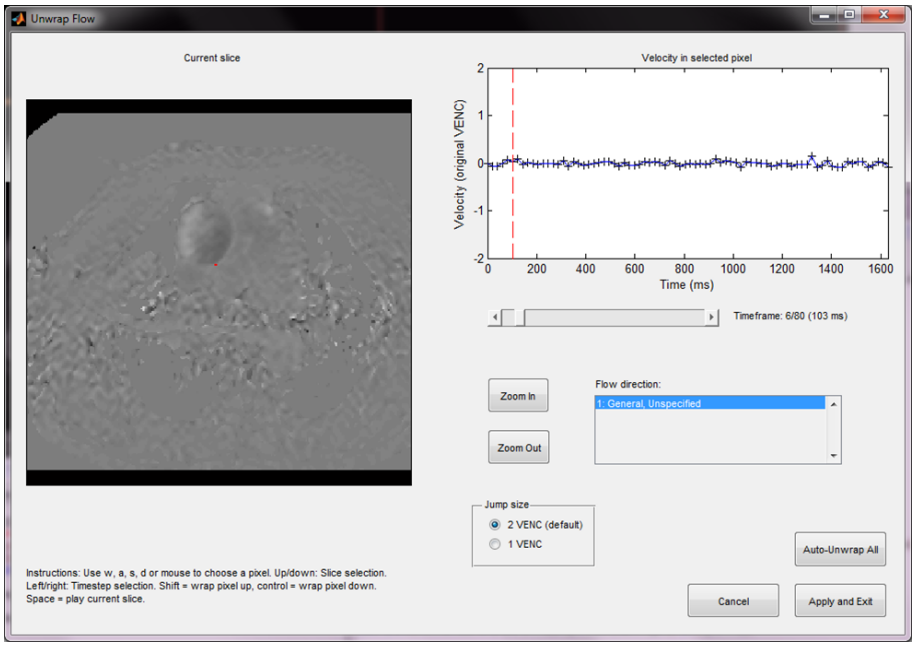


Figure 38: Example of the graphical user interface for phase unwrapping. The left image panel shows the original phase, and the right image panel shows the unwrapped phase. The long slider adjusts the current time frame.

23.5 Creating angio and velocity magnitude images

It is possible to create a so called angio image that is the magnitude image times the velocity magnitude. This is available under the Flow menu and Create Angio. If you have more than one velocity encoding direction it is possible to create a velocity magnitude image that is the square root of the sum of squares of all velocity directions (velocity magnitude).

23.6 Coupling magnitude and flow images

If magnitude and flow image stacks have been loaded into Segmentwithout being coupled to each other, it is possible to couple them using the Couple Magnitude/Phase Flow Image Stacks from the Flow menu. Available magnitude and phase image stacks are then identified and coupled using heuristics.

24 Pulse Wave Velocity Analysis

The functions described in this chapter is in US only for off label use and for investigational use.

An overview of the Pulse Wave Velocity module is shown in Figure 39. Upon launch, the module automatically finds the image stack that contains a measurement labelled `Aortic Length` and the two flow image stacks that contain ROI's labelled Aortic ascending flow and Abdominal aorta. The image on the left of the GUI shows the image containing the measurement. This measurement is displayed in yellow and the intersections with images containing flow are displayed as white lines. The plot on the right side shows the flow curves of the Aortic ascending flow ROI (in blue) and the Abdominal Aorta (in red). For each flow curve, the tangent of the upslope is calculated using a Gaussian smoothing function and displayed as a dashed line in the corresponding color. The sigma parameter of the smoothing function can be adjusted using the slider on the right of the plot.

Pulse wave velocity is calculated using the length of the Aortic Length measurement and the time between the upslopes of the flow curves. The time is measured as the temporal distance from the moment when the tangent of the Aortic ascending flow curve is equal to zero to the moment when the tangent of the Abdominal Aorta curve is equal to zero. This distance is displayed as a dotted portion of the black line along y = 0 in the plot. The values for aortic length, time between upslopes and calculated velocity are displayed in the GUI and can be exported to a spreadsheet by clicking the Export button.

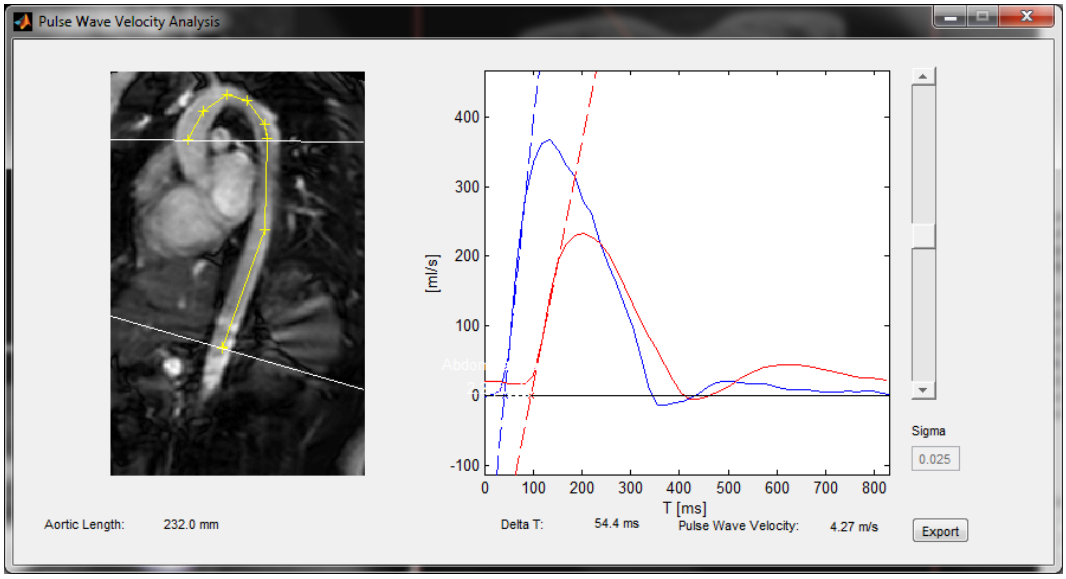


Figure 39: GUI for Pulse Wave Velocity Analysis. On the left is the image containing the measurement of Aortic Length. On the right is a plot of flow curves along with their respective tangents.

25 Stress Analysis

In earlier versions of Segment there were a special stress viewer available. This have been removed since it's functionality is now directly available in the normal viewing capabilities of Segment (synchronized viewing of several image stacks). It is possible to place four (or more) image stacks on the screen simultaneously and play them synchronized in the same speed by the icon . Other functionality in Segment that could be used to analyse stress images is the report per slice functionality, described in Section 26.2 which allows quantitative studies of wall motion abnormalities.

Further hints on doing stress analysis is to label your image stacks. Then it is easy for the viewer to see which image stack is stress and which is rest. This is done by right click on the image thumbnail and select Set Image Type in the pop-up menu.

26 Regional Wall Analysis

There are a number of different analysis options available to make regional wall analysis. Please note that for regional wall motion analysis the common clinical practice is to exclude the papillaries from the segmentation, for more information on how to include/exclude the papillaries, see Section 12.3.

There are three different visualization options available for wall motion analysis:

- Radial contraction versus time
- Report per slice (icon)
- Bullseye plots (icon)

26.1 Radial contraction versus time

In this option the regional contraction velocity per segment is plotted over time. On the y-axis on each plot is the slices (basal to apical), and on the x-axis is time. An example is shown in Figure 40.

26.2 Report per slice

It is possible to do regional wall motion analysis on a slice by slice basis. This tool is started by the icon . Possible parameters to plot are wall thickness, fractional wall thickening, radial contraction velocity, and radius. An example showing wall thickness over time is shown in Figure 41. You can adjust the start of the sectors by using the rotation slider or take the starting sector as the sector that is closes to the annotation point `Start Sector`. How to place annotations, see Section 19.7.

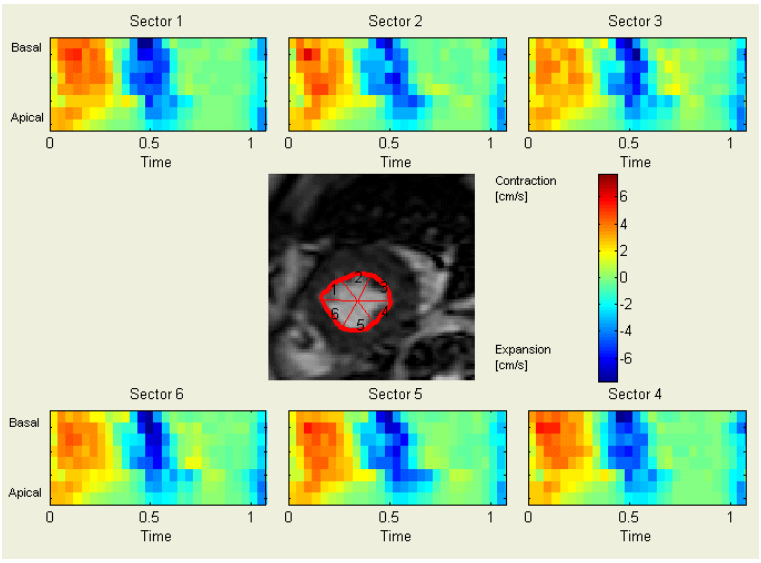


Figure 40: Radial velocity versus time in six sectors. Note the apical to basal gradient in the onset of the radial contraction.

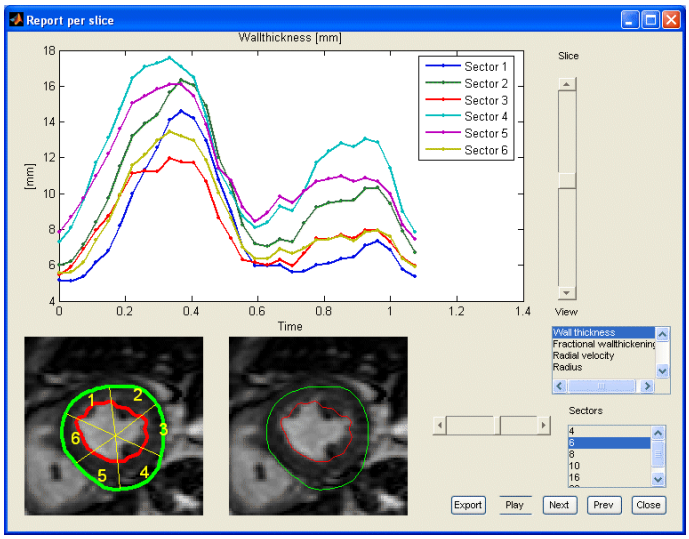


Figure 41: Wall thickness over time in a healthy subject.

27 LV Sphericity Analysis

LV sphericity can be calculated from the Report menu.
The sphericity of the left ventricle is defined as the maximum short-axis diameter divided by the length of the ventricle. This calculation is performed separately for ED and ES and for each of these timeframes, it is required that there exists LV endocardium segmentation in an open short-axis image stack, as well as an image stack containing a measurement labelled End Diastolic Length and End Systolic Length respectively.

The values of diameter and length of the ventricle and the calculated sphericity are displayed in a messagebox and copied to the clipboard, allowing the user to paste them into a spreadsheet.

28 Export Images and Results

There are many options to do batch exporting from multiple `.mat` files. Please see Chapter 20 for further details.

28.1 Export results to clipboard

These functions export results such as LV mass, ejection fraction, volumes etc, to the clipboard. Data is outputed in a format so that it directly can be pasted into Microsoft Excel (by usage of `Ctrl-V` in Excel) or other spread sheet softwares. When you need to export data from multiple files, it is strongly recommended to use the utility to summarize `.mat` files described in Section 20.10.

28.1.1 All stacks with header

This function exports the results of all image stacks and includes a header line above. Segment tries to use the image type to determine which image stacks are short axis cine images which are used for mass and ejection fraction, flow image stacks, delayed enhancement image stacks and so forth.

28.1.2 All stacks

Same as above but no header line is included in the output.

28.1.3 This stack with header

This function only outputs results from the current image stack and includes a header line.

28.1.4 This stack

Same as above but without including a header line.

28.2 Export volume curve to clipboard

The volume curve (both) endocardial volume, and epicardial volume is copied into two columns.

28.3 Export contour to clipboard

This function ask what contours to export and export the internal representation to the clipboard. You can currently chose to export LV endo-, epicardium, RV endo- and epicardium, respectively.

28.4 Export volume of contours per slice

This function export the volume of each contour per slice. Data is exported for all contours and all time frames. If you instead want to have the area per slice you can divide the result with the slice thickness in cm to get the area in cm^3.

28.5 Export image

Using this option, only the current frame without segmentation is exported as a file. You need to select file format, and the following formats are supported: `.jpg`, `.bmp`, `.png` (portable network graphics), and `.tiff`. The recommended image format to use is `.png`.

28.6 Export screenshot

Using this option, the current frame including segmentation is exported as a file. The following image formats are supported: `.jpg`, `.bmp`, `.png` (portable network graphics), and `.tiff`. The recommended image format to use is `.png`. There is also an option to save the screenshot file to a PACS system.

When preparing images for publication it is often helpful to change the color of the contours to black/white and increase line width to increase visibility. This can be done under the preferences menu, see Chapter 29 for further details.

28.7 Export movies

Exporting movies can be done by either using the built-in movie recorder in Segment or by exporting the current image stack as a movie (Export Movie).

28.8 Movie Recorder

This is an experimental functionality that take screen captures and store them in a movie format. The movies can be done in two ways and either to `.avi`-files or a sequence of `.png` files (that later can be converted to different file formats). In future versions it will also be possible to export to animated `.gif` format. You can create movies of the main view, zoom view, 3D plot view, report per slice view. First select Movie Recorder under the Export menu. This brings up a user interface shown in Figure 42.

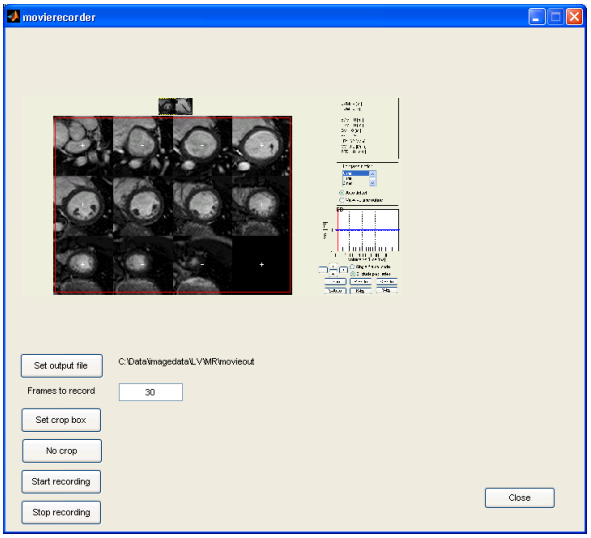


Figure 42: Movie Recorder GUI.

The movie recorder is when started unpopulated. To do a first screen capture force an image update by view next frame. You can now set a crop box (shown in Figure 42 as a red box), set number of frames to record, and start to record the movie. Usually you should set the number of frames to record to the same number of time frames as there are frames in the image stack. When all frames are recorded then a file selection pop up menu appears and where you can select storing options. When exporting to `.avi` files you need also to select a movie compressor, since all compressors might not be available on your computer. Personal experiences are that the cine-pak encoder are pretty stable.

29 Customizing Segment

This chapter describes how to customize Segment. It is recommended to set the preferences of which folders to use to avoid browsing each time you want to load or save a file. The GUI for setting preferences is shown in Figure 43. It is invoked by using the menu Preferences on the main menu.

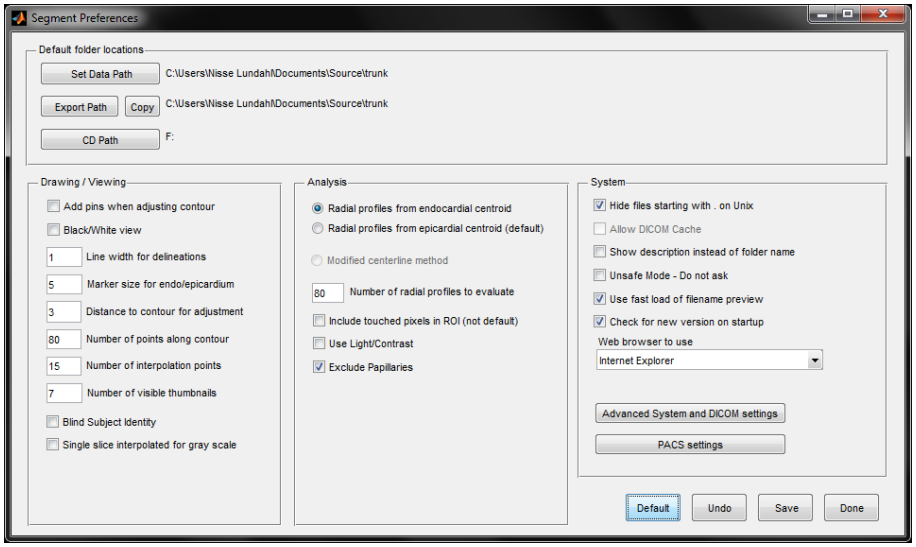


Figure 43: Preferences GUI.

There are four panels in total. The top most panels sets default folder locations for loading, and saving, respectively. It is also possible to indicate which drive / path that corresponds to your CD-drive. Then, the left most panel sets preferences for editing and drawing contours, the middle panel sets preferences for regional analysis, and the right most panel sets system preferences. The button Advanced System and DICOM Settings opens a new interface with settings for base image path for patient database, and DICOM communication parameters. The button PACS Settings opens an interface with settings for PACS communication.

The option ☒ Add pins when adjusting contour controls weather points should be

placed when manually correcting a contour. This option should be checked when modifying time resolved images, but unchecked otherwise. ☒ Black/White view plots the endocardium and epicardium with white lines. This is useful for making screen captures for illustrations that are not printed in color. The edit box `Line width for endo/epicardium` sets line width for the contours. This again is useful for making screen captures. Default line width is 1. The edit box `Distance to contour for adjustment` adjust how close to a contour one need to click before this contour is activate. When using the interpolate tool it is recommended to set this to quite small, typically 1-2. The edit box `Number of Points Along Contour` sets the number of points that are stored along a contour for endocardium and epicardium. When using automated segmentation this value should be set to 80. When manually drawing complicated objects this can be set to a higher number.If the option ☒ Blind Subject Identity is checked then the program will not show patient info on screen this is useful for making screen shots etc for presentations. It is highly useful when doing research and the observer should be blinded to the patient identity. The edit box `Number of visible thumbnails` sets the maximum number of thumbnails visible. When the number of image stacks exceeds this number a slider will be visible to scroll through all the thumbnails.

The radio buttons `Radial profiles from endo/epicardial centroid` controls how regional wall measures are placed. The radio button ◎ Modified centerline method is reserved for future use when the modified centerline method will be implemented. The edit box `Number of radial profiles to evaluate` sets the number of radial spikes that are evaluated before sector means are calculated. For more details on how the regional parameters are calculated see Chapter 44. The checkbox ☒ Include touched pixels in ROI sets how the edge pixels of a ROI are treated. When selected all pixels that are touched by the ROI are included. The default behavior is to include only the pixels where the center of the pixel lies within the ROI.

The checkbox ☒ Allow DICOM cache allows creation of cache files for tags in DICOM files to be generated.

The web browser to be used can be chosen in the drop list by either choosing a program if it is installed in the default location or choose other to browse for the program file to use for example select `chrome.exe`, or `firefox.exe`.

Customization of the Report Module is described in Chapter 38.

29.1 Image description settings

The automatical definition of image description parameters upon loading is controlled by a parse file. A schematic view of the parse file is shown in Figure 44.

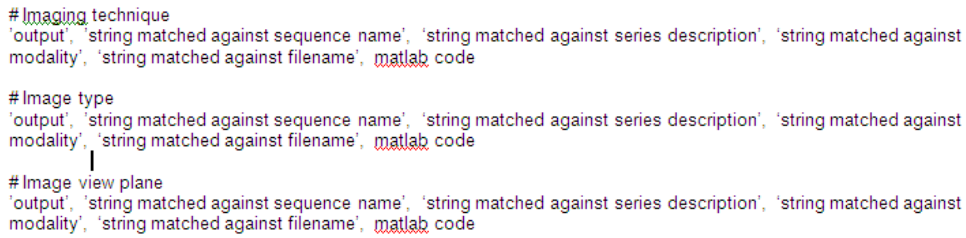

Imaging technique
'output', 'string matched against sequence name', 'string matched against series description', 'string matched against modality', 'string matched against filename', matlab code
Image type
'output', 'string matched against sequence name', 'string matched against series description', 'string matched against modality', 'string matched against filename', matlab code
Image view plane
'output', 'string matched against sequence name', 'string matched against series description', 'string matched against modality', 'string matched against filename', matlab code

Figure 44: Schematic view of the parse file for image description settings.

Correctly defined image description parameters is important in the use of automatic analysis tools. The image description is divided into three parameters; Imaging technique, Image type and Image view plane. The definition of image description parameters is controlled by manually change the parse file imagedescption.tex according to Figure 44. This make it possible to adjust the definition of image description parameters to different acquisition parameters settings. There are no limitations in the number of specifications below each image description parameter. An example of a parse file is shown in Figure 45. If you have questions, please contact `support@medviso.com` for further details.

29.2 Advanced and DICOM Settings

The graphical interface for advanced settings is shown in Figure 46. The GUI is divided into four sections; Database settings; Segment Server settings; Sending DICOM files; and DICOM interpretation.

```
#Image type
General,,,,,
Perfusion Rest,,rest,,,
Perfusion Rest,,,,REST,
Late enhancement,,DE,,,
Late enhancement,,Viabilitetm3d,,,
Late enhancement,,3D viab,,,
Cine,,sbFE,,,isempty(SET(no).Flow)
Cine,,M2D,,,

#Image view plane
Unspecified,,,,,
2CH,,2ch,,,
3CH,,3ch,,,
4CH,,4ch,,,
Sagittal,,sag,,,
Coronal,,cor,,,
Frontal,,front,,,
Transversal,,trans,,,

#Imaging technique
Unspecified,,,,
MRSSFP,,SSFP,,,
MRSSFP,,tf2d,,,
MRSSFP,,fiesta,,,
MRDE,,DE,,,
MRDE,,psir,,,
NM,,,NM,,
PT,,,PT,,
CTheart,,,CT,,
US,,,US,,
```

Figure 45: Example of a parse file for image description settings.

In this section we will only describe DICOM interpretations the other settings are explained in conjunction with Segment Server documentation, and Patient Database Module.

The DICOM interpretation adjusts how Segment interprets DICOM files. The checkbox ☒ Force 16 bit DICOM enforces Segment to assume usage of 16 bit DICOM files, regardless what is stated in the file. This option is helpful when images looks like chessboard when read into Segment. For further details see about loading DICOM files in Chapter 9.

29.3 PACS Settings

PACS Settings are described in the Segment Database Manual.

29.4 Technical details

On Windows platform, the preferences are stored under the local user folder and the subdirectory `Application Data/Segment`. This means that each user have can set their own preferences. If you want to have it setup so that all new users on the computer will have a default setting of preferences, then

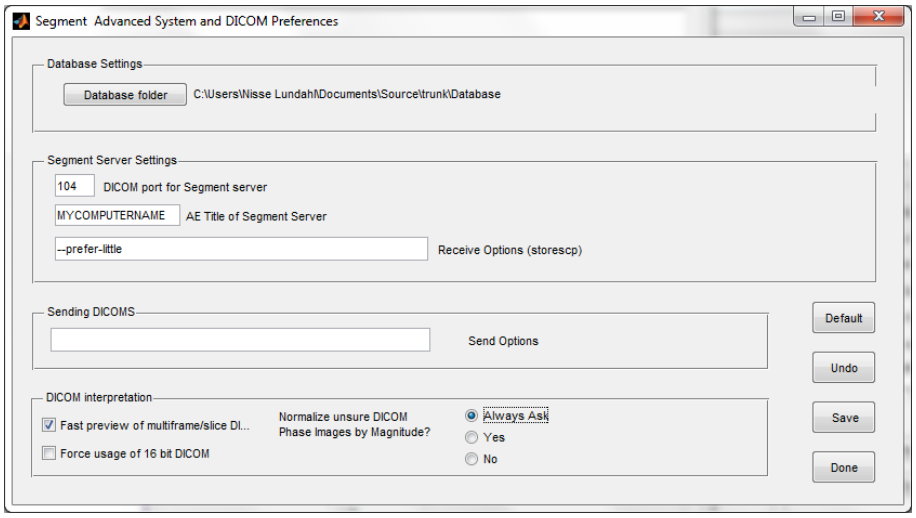


Figure 46: Advanced and DICOM Settings GUI.

copy the `preferences.mat` from one user to the folder where Segment is installed. Finally make this file write protected. In the preferences folder Segment also stores a log file for debugging purposes, and small temporary files that are used in the PACS communication batchdownload process.

30 Image Reformat (MPR)

The functions described in this chapter is in US only for off label use and for investigational use.

It is possible to reformat an image stack along any axis. The main purpose of this tool is to be able to resample the data volume to short axis slices (if they are for instance scanned in an axial direction). The reformater can also be used to construct a long-axis image from a stack of short-axis slices. The user interface is shown in Figure 47.

One limitation with the multiplanar reconstruction is that it does not utilize the patient image coordinate system. This means that image stacks created with the reformater does not display image plane crossings. This will be addressed in future versions of Segment. Furthermore, the MPR routine does not currently support non-isotropical voxels (i.e voxels of dimension 3x4x8 mm). Voxels where x and y size are equal do work, i.e 3x3x8 mm works fine.
The functions are:

New cut	Resamples into parallel slices to the selected line. The cuts are also perpendicular to the viewing direction.
Previous cut	Backs up one level in the cut history. The current cut is not saved.
Done/Export	Exports the resample image stack back to Segment.
Play	Then this toggle button is selected then the image is played as a movie.
Close	Closes the dialog resampler without storing any information.

Parameter slice determines the slice distance in mm, and output determines

the output resolution in the new 'short-axis' plane.

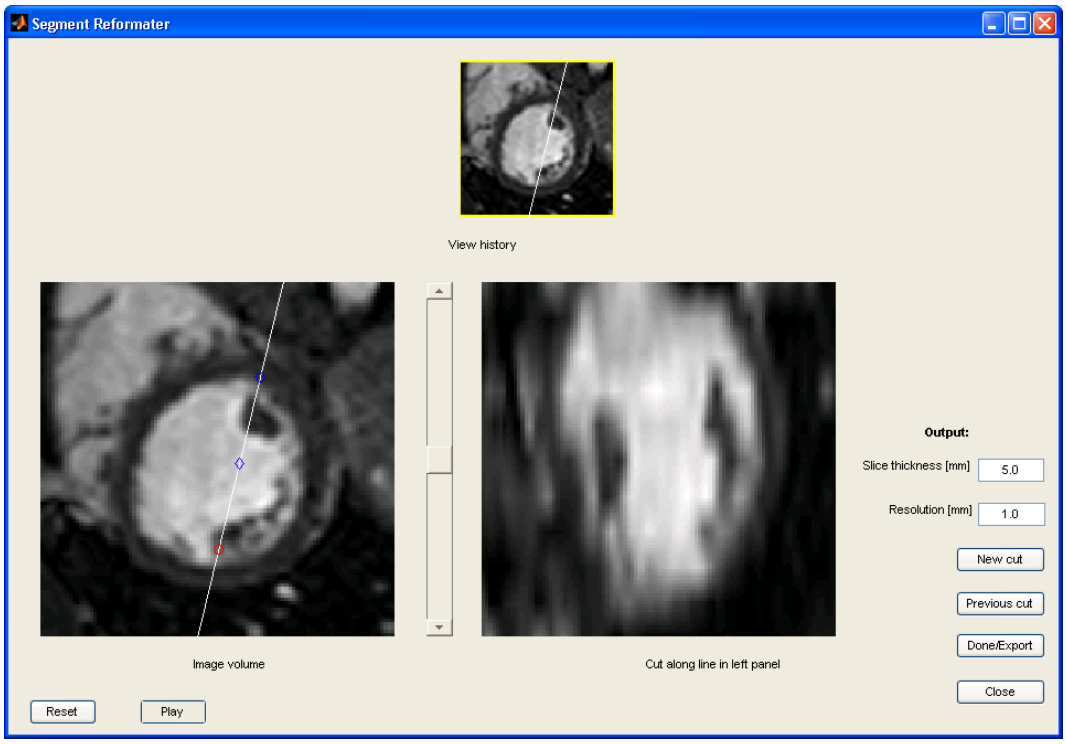


Figure 47: Image reformater GUI.

31 T2/T2* Quantification Module

The functions described in this chapter is in US only for off label use and for investigational use.

In magnetic resonance (MR) imaging, T1, T2 and T2* relaxation times represent characteristic tissue properties that can be quantified with the help of specific imaging strategies. The purpose of the T2/T2* Module is to quantify T2 and T2* relaxation times in MR imaging. Quantification of T2 and T2* values follows the same underlying mathematical principles, but different source images are used.

T2* changes have been shown and quantified under pharmacological test in coronary artery disease [11], quantification of iron overload and of the heart and liver in Thalassaemia major [12].

T2* values can be quantified by varying when the same image is acquired using different echo times.

31.1 Module overview

An overview of the T2/T2* quantification module is shown in Figure 48. The top left image panel shows the magnitude images for the different echo times, adjustable with the echo time slider. The lower left panel allows to make regional restriction on what regions to quantify. There are three modes and in the first mode Use only myocardium the pixels inside the myocardium is included in the quantification. The second mode Use only ROI includes only pixels that are inside region of interests. In the last mode Use full image all pixels are included in the quantification. The delineation of ROI's and myocardium is taken from the last time frame in the image series. The right image panel shows the pixelwise T2* values.

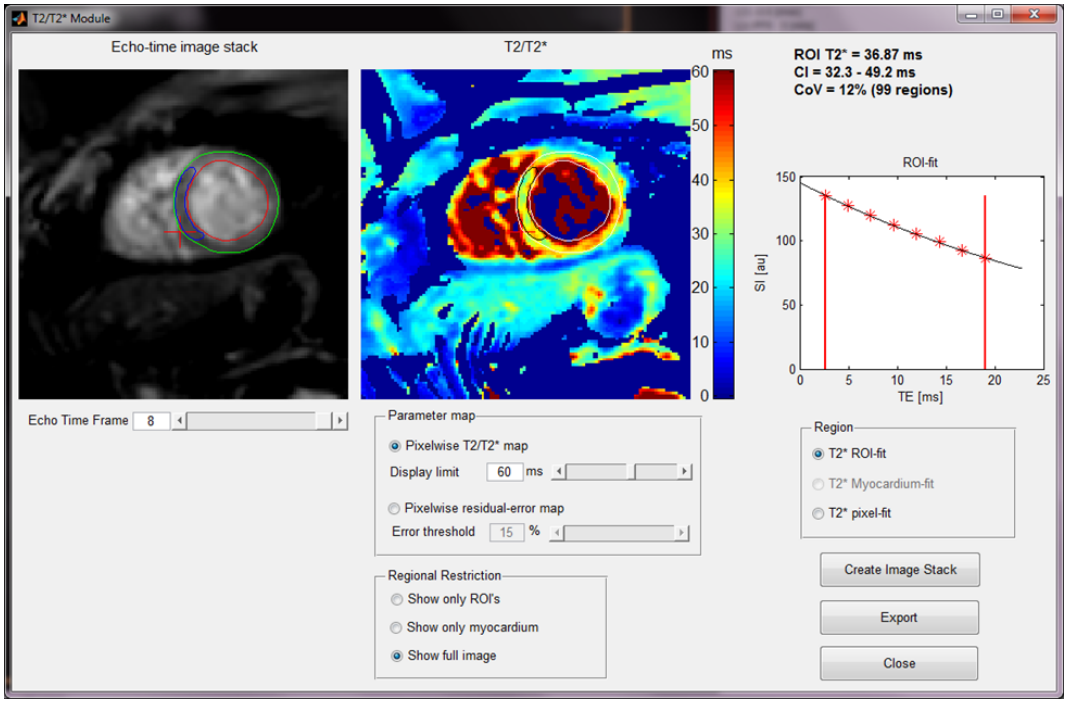


Figure 48: GUI for quantification of T2/T2* values. The top left image panel shows the magnitude images for the different echo times, adjustable with the echo time slider. The right image panel shows the pixelwise T2* values.

The right lower panel shows the fittig curve over time. The mean T2* value is presented in the graph and the associated graph title. The region for the mean value calculation is according to the selection of the checkboxes to the right, either `T2* ROI-fit` or `T2* pixel-fit`. The T2* pixel-fit takes the T2* values according to the blue cross in the right image panel.

T2* values can be exported to spreadsheet by using the Export button. To create the T2* image stack in the main GUI of Segment use the Create Image Stacks button.

31.2 Implementation

The detailed implementation of the T2/T2* calculation in given in Chapter 44. In short the calculation is performed with standard exponential curve fitting that is calculated in the least square sense.

31.3 Validation

The module has been validated comparing to the open source software MRmap [13]. More validation details is available in a separate report from Medviso AB.

32 SPECT Analysis Module

The functions described in this chapter is in US only for off label use and for investigational use.

The SPECT Analysis Module is work in progress and therefore are not all automatic analysis tools currently freely available. The SPECT analysis module can be used in both gated and non-gated image stacks for analysis of left ventricular mass and volumes, quantification of stress-induced ischemia, myocardial infarction and myocardium at risk. To use the automatic analysis tools, the `Imaging Technique` has to be defined as NM.

32.1 Visualization

In addition to the regular view of image stacks within Segment there are two visualization views specific for SPECT images. By using Plot 2D View under the SPECT menu a seperate graphical user interface is opened with three short-axis slices (one basal, one midventricular and one apical slice) and horizontal and vertical long-axis projections. The user interface is shown in Figure 49. In the left panels the stress image stack are shown and in the right panels the rest image stack. For Segment to be able to identify the rest and stress image stack, the `Image Type` has to be defined as Perfusion Stress and Perfusion Rest, respectively. By using the + and - buttons in the lower panel the LV segmentation for each image stack can be manually corrected by include / exclude basal or apical SA-slices in the LV segmentation. For gated image stacks the visualization is time resolved and the left ventricular blood volume is illustrated as a curve over time to the right in the interface.

A three dimensional view of the counts within the LV myocardium is presented by using Plot 3D Surface under the SPECT menu. This will open a separate graphical user interface, shown in Figure 50.

32.2 Automatic segmentation of the left ventricle

The function Auto Delineate LV under the SPECT menu automatically segment the left ventricle in the current image stack. To use the function the

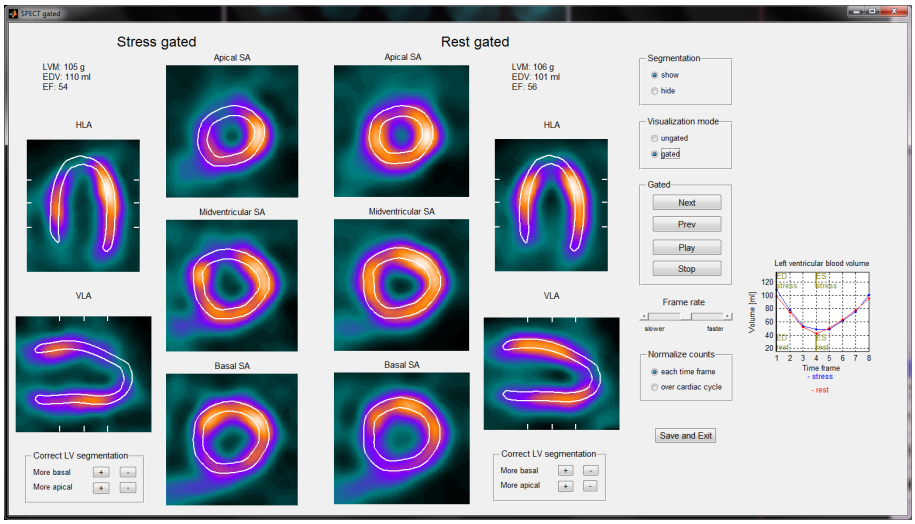


Figure 49: Graphical user interface of the 2 dimensional visualization for SPECT images.

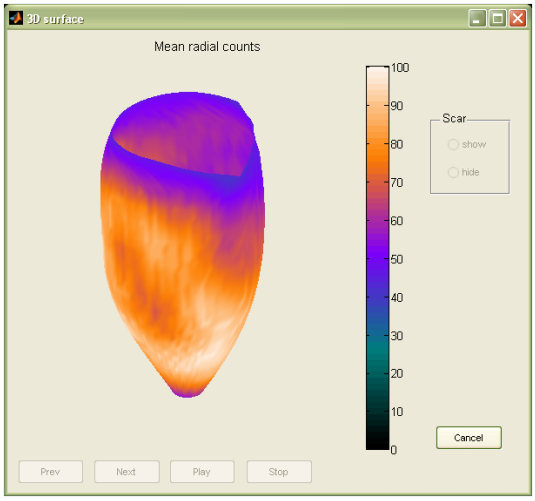


Figure 50: Graphical user interface of the 3 dimensional visualization for SPECT images.

image stack must fulfill the following requirements.

- The image stack need to be in short-axis projection.
- The "Number of points along the contour" must be greater then or equal to 50 (define in the Preferences menu).
- The slices have to be in the order basal to apex when go through the slices from the top to the bottom. If this requirement is not fulfilled use the function Flip z (also Flip in x) under Flip & Rotate→Image tools.
- The septal part of the heart have to be in the left side of the image.

A segmented left ventricle is shown in Figure 51. The endocardial segmentation is illustrated as red lines and the epicardial segmentation as green lines.

32.2.1 Manual corrections

If the results from the automatic left ventricular segmentation algorithm is not satisfying, the user can do manual corrections. This can be done in four ways:

- Crop the image stack using the icon (find in the lower right panel in the main interface). If there are extra-cardiac activity this can affect the segmentation.
- Manually select short-axis slices for the LV segmentation. This is done by select the slices in question for the segmentation by using the icon (find in the lower right panel in the main interface).
- Manually point out the center point of the left ventricle. Use the icon (find in the lower right panel in the main interface) and place two points in the middle of the left ventricle in two different image slices. The program then adjust a center point line through all slices by adjusting a straight line to these two center points. It is important that it is just two points because otherwise the segmentation algorithm ignores them and automatically select center point.
- Manually change the finished segmentation with the pen for endocardium segmentation and epicardium segmentation .

32.3 Automatic quantification of myocardium at risk

To perform automatic segmentation of the myocardium at risk (MaR) in the segmented left ventricle use the function Auto Detect MaR under the Myocardium at Risk and SPECT menu. The MaR in the SPECT image are defined as a region with low intensity. The intensity limit that define the perfusion defect are set by the MaR preferences, as described in the next section. An example of outlined MaR are shown in Figure 51. From the segmentation, the MaR is quantified by percentage extent, absolute volume in ml, severity of the defect and total perfusion deficit (TPD). The TPD value includes both extent and severity of the MaR and ranges between 0 (no perfusion defect) to 100 (severe perfusion defect in the whole LV).

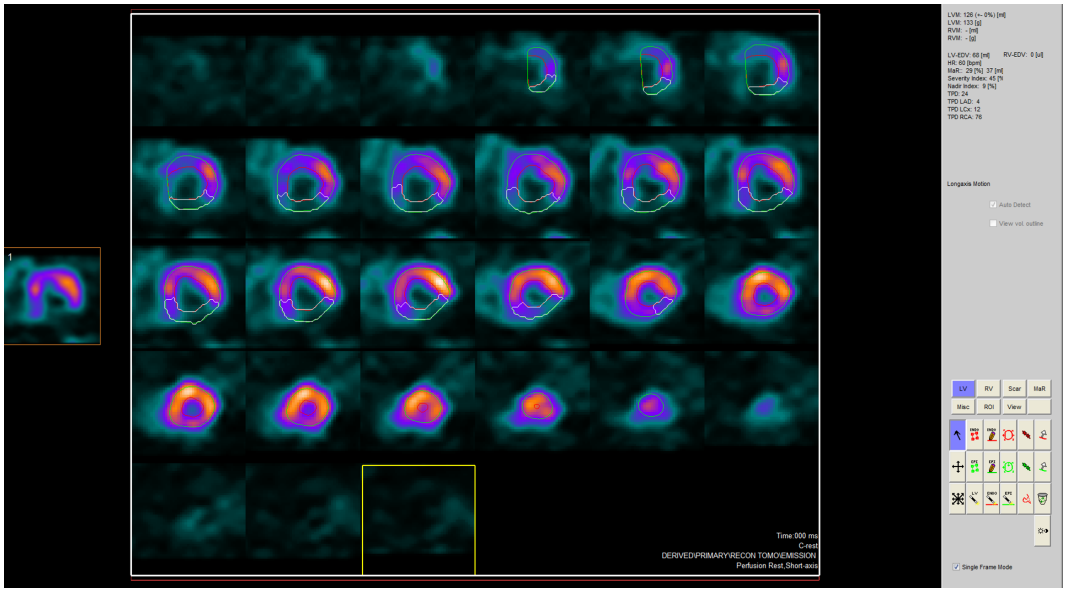


Figure 51: An example of a segmented left ventricle with myocardium at risk outlined. The red line is the endocardium, the green line the epicardium and the yellow line the perfusion defect.

32.3.1 Define RV center

In order to calculate the TPD value for each of the sections of the LV supplied by the three main coronary arteries (LAD, RCA, and LCx), the placement of

the right ventricle in relation to the left ventricle need to be defined. This is done by estimating the RV center straight to the left of the LV center. This estimation can then be corrected manually in the interface shown in Figure 52. The RV center definition is performed as one step in the quantification of myocardium at risk. In the interface, use the button "Set manually" to correct the RV center definition and the button "Confirm" when the RV center definition is sattisfying.

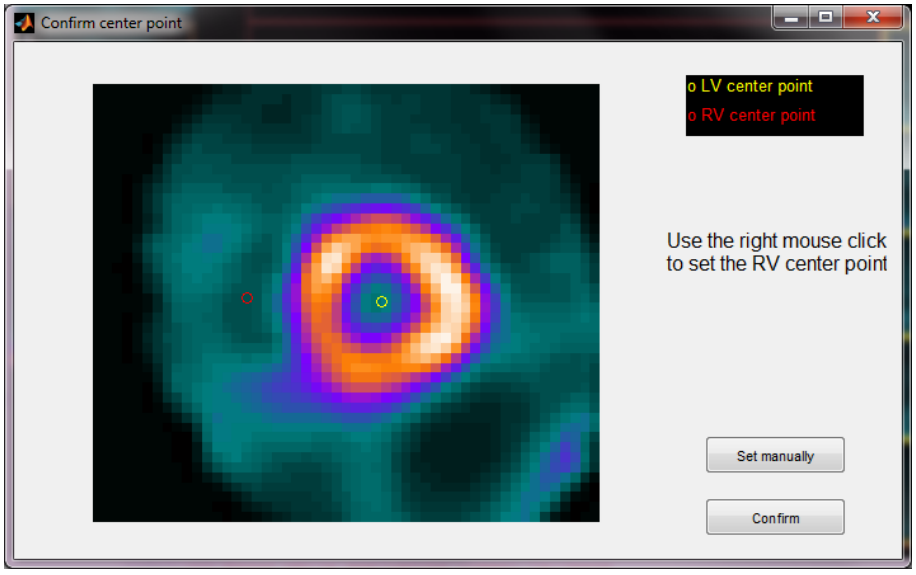


Figure 52: The interface for definition of the right ventricular center point.

32.3.2 Set preferences

The MaR preferences are set by the function Set MaR preferences under the Myocardium at Risk and SPECT menu. The preferences are set for each image stack which make it possibly to have different preferences for different image stacks.

The MaR preferences interface is shown in Figure 53. The choice made in the upper panel determine the region for which the count calculations are done in. The two selections are ROI (the default value) and Image. The Image selection include all pixels in the image in the defect calculation while

the ROI selection only include the pixels within the LV segmentation in the calculations. The "Count Maximum" number is defining the percentile (the default value is 100%). The "Threshold" number is determined the percent of Count Maximum which defined a defect (the default value is 55%). All pixels with a count lower than this value are included in the MaR segmentation process. The "Minimum volume" number determined the smallest volume for a defect, expressed as percentage of the LVM (the default value is 10%). All defects with a volume smaller than this number are excluded from the MaR segmentation. The two selection for the subdivision of the LV used in the a priori model are the default model (based on normal coronary artery perfusion territories) and the standard 17-segment model. The choice in the lowest panel determine if the a priori model of the coronary distribution should be used in the MaR segmentation or not.

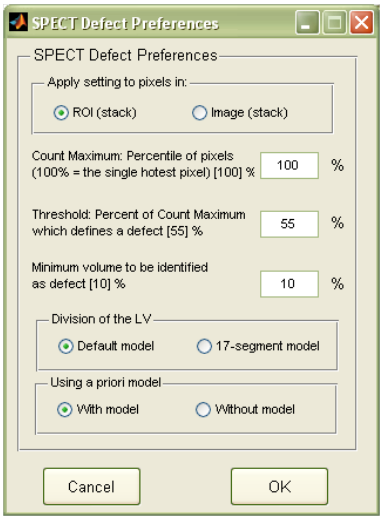


Figure 53: The MaR preferences interface.

32.3.3 Reset MaR

To reset the MaR quantification use the function Reset MaR under the Myocardium at Risk and SPECT menu. This function reset both the MaR segmentation and the MaR preferences for the current image stack.

32.4 Perfusion analysis

The automatic analysis of myocardial perfusion is work in progress and will be made freely available upon publication of these algorithms.

32.4.1 Automatic quantification of stress-induced ischemia and infarction

To perform automatic quantification of stress-induced ischemia and infarction both a rest and stress image stack need to be present. For Segment to be able to identify the rest and stress image stack, the `Image Type` has to be defined as Perfusion Stress and Perfusion Rest, respectively. The automatic quantification of stress-induced ishcemia and infarction in SPECT images is performed by two steps. First, an image registration is performed between the rest and the stress image stacks. Secondly, segmentation and quantification of the perfusion defects is performed by using the rest and stess counts, the stress-rest count change and the rest wall thickening (if a gated rest image stack is present). The following sections describe the two steps.

Image registration

The image registration between the rest and the stress image stacks is performed by use the function Auto Image Registration under the Perfusion and SPECT menu. The registration method is based on statistical optimization and the result can therefore vary slightly each time registration is performed on the same image stacks. To only show the registration result, use the function Show Image Registration under the Perfusion and SPECT menu. Figure 54 show the result by the automatic registration algorithm. From the interface, it is possibly to manually correct the registration by using the tools to the right in the interface. To reset the manual corrections and go back to the automatic registration, use the button "Reset registration" in the interface. To continue with the automatic perfusion analysis, use the button "Perfusion analysis".

Segmentation and quantification

The quantification of stress-induced ischemia and infarction is performed by using the function Auto Perfusion Analysis under the Perfusion and SPECT menu. A pre-request to perform perfusion analysis is image registration

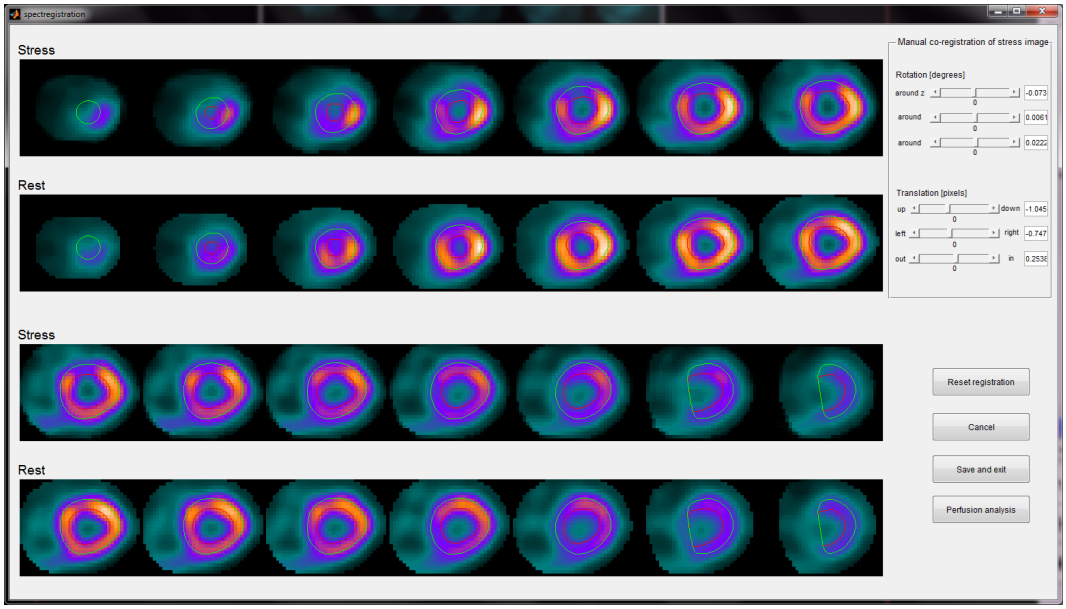


Figure 54: The rest-stress registration interface.

between rest and stress image stacks, as described in the previous section. Figure 55 illustrate the interface for showing the perfusion analysis result. The defect quantification is presented for both the rest and the stress study as well as for the stress-rest change. The rest defect is the quantification of myocardial infarction and the stress-rest change is the quantiafication of stress-induced ischemia. The defect quantifications are presented both as percentage extent of the LV, absolute volume in ml and by Total perfusion deficit (TPD). TPD is a measure of the perfusion defect including both the extent and the severity of the defect. It is presented for the whole LV as well as for each of the three coronary arteries (LAD, LCx, and RCA). To be able to calculate the TPD for LAD, LCx and RCA, the RV center need to be defined. This is done as described in the previous section "Define RV center".

32.4.2 Automatic quantification of stress perfusion defect

When there is only a stress MPS image stack present, the perfusion analysis tool (Auto Perfusion Analysis under the Perfusion and SPECT menu) can only

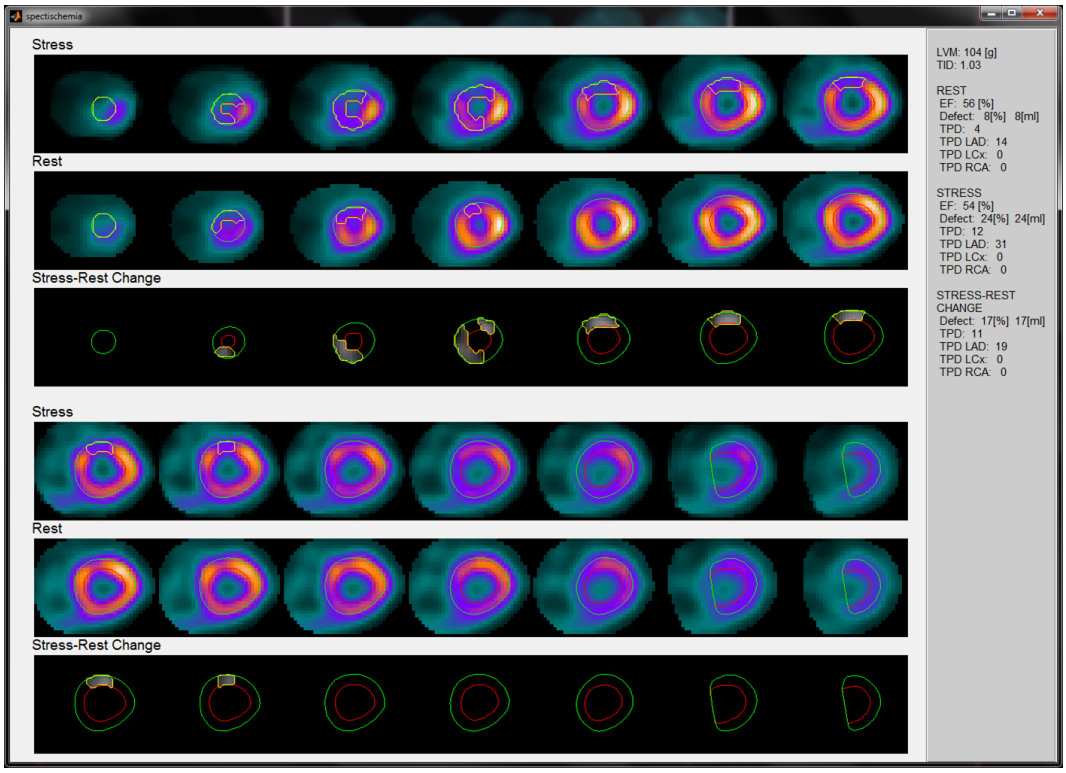


Figure 55: The perfusion analysis interface. The red line is the endocardium, the green line the epicardium and the yellow line the perfusion defect.

quantify stress perfusion defects. The automatic quantification is performed by using the counts in the stress image stack and the result is illustrated in an interface similar to the interface shown in Figure 55. The defect quantification is presented both as percentage extent of the LV, absolute volume in ml and by Total perfusion deficit (TPD). TPD is a measure of the perfusion defect including both the extent and the severity of the defect. It is presented for the whole LV as well as for each of the three coronary arteries (LAD, LCx, and RCA). To be able to calculate the TPD for LAD, LCx and RCA, the RV center need to be defined. This is done as described in the previous section "Define RV center".

32.4.3 Manual perfusion scoring

Segment provides an inferface for manual scoring of tracer uptake and myocardial infarction. The inferface is illustrated in Figure 56. The scoring is performed for each of the segments in the AHA 17 segment model. Summed scores are calculated for stress (SSS), rest (SRS) and stress-rest difference (SDS). There are two modes for the scoring, the first illustrating the rest and the stress ungated images and are for scoring of the tracer uptake. The scoring values should be between 0 and 4 as described to the right in the interface. The second scoring mode is found by choosing "gated" under the Visualization mode. This opens the interface for scoring the precens of myocardial infarction. For this pupose, the rest gated and ungated image stacks are used and the scoring values should be between 0 and 2 as described to the right in the interface.

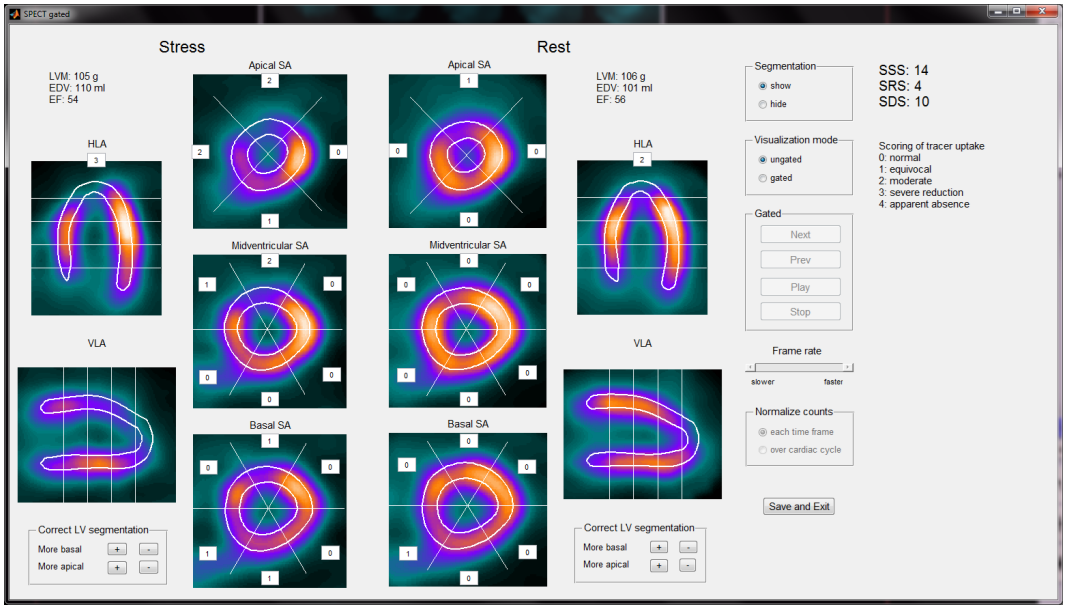


Figure 56: The perfusion scoring interface. The LV is divided into 17 segments accoring to AHA model.

33 Cardiac CT Module

The functions described in this chapter is in US only for off label use and for investigational use.

Currently we are working on a Cardiac CT Module that will be useful for automated segmentation and image analysis of CT images. Currently this functionality is only available upon request.

In the module functionality for automatic segmentation of pericardial sac (whole heart CT), automatic identification of the coronary ostia, and automated bone segmentation. The automated segmentation of the pericardial sac will be highly useful for visualization of the coronary arteries in conjunction with the volume rendering module that is work in progress.

Please contact Medviso AB to get a demo of these features.

34 Strain Analysis Module

The functions described in this chapter is in US only for off label use and for investigational use.

34.1 Velocity Encoded Imaging

The strain analysis module uses velocity encoded MR images to calculate myocardial strain. The module have been written by Helen Soneson as her Master thesis work [14], and resides on the work by Erik Bergvall for strain calculations and myocardial tracking [15]. This module is not available yet to researchers since it is under development and will be released as soon as the underlying method is properly published. Preliminary results about the method was presented at SCMR 2008 [16],[17].

Strain calculations require velocity encoded MR images with two velocity components. An example of such an image stack are shown in Figure 57. The leftmost panel is the magnitude image stack the two rightmost are the velocity image stacks.

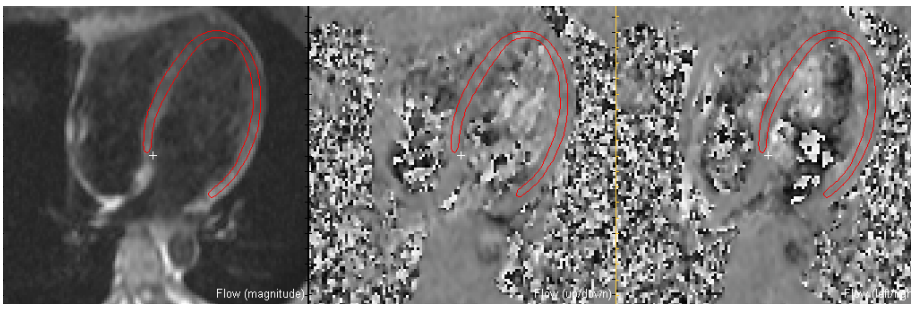


Figure 57: Example of a velocity encoded magnitude image stack and two directional velocity encoded image stacks.

Before starting strain calculation the myocardium of the left ventricle need to be manually outlined in end-diastole. One method to do this is to use the endocardium tool directly in the velocity encoded image stack. One tip before outline the myocardium in a long-axis image is to first set the

"Number of points along the contour" in Preferences under the Preferences menu to 300. This make it easier to do small changes in the segmentation. The other method is to segment the myocardium in the anatomical (balanced or SSFP) image stack and then exported it to the velocity encoded image stack. The exportation is done with the function Import From Cine Stack under the menu Strain From Velocity Encoded Imaging under the Strain menu. Before calculating strain the image type have to be set to either "Strain 2CH TFE" or "Strain 2CH FFE" (and similar for 3CH and 4CH). This is done either upon loading or by right clicking on the corresponding thumbnail images and select Set Image Type.

34.1.1 Strain calculation

The strain in a long-axis velocity encoded image stack is calculated by using the function Strain Tool under the Strain From Velocity Encoded Imaging under Strain menu. Note that you need to manually outline the myocardium in end-diastole first. The function calculates segmentation and strain in all time frames. It also opens a new graphical user interface that make it possible to analyse/visualize strain in the image. An example of such a GUI can be seen in Figure 58.

To select which strain or displacement parameter to analyse, mark one of the parameters in the listbox in the figure. The 4 alternatives are:

- Total Strain
- Radial Strain
- Longitudinal Strain
- Shear Strain

To see how strain changes over time there are three buttons in the figure to use. Prev that step one time frame backward in the heart cycle. Next that step one time frame forward in the heart cycle and Play plays a movie of strain over the whole heart cycle. The buttons Min and Max produce a figure of minimal respectively maximal strain in each pixel over time.
The Export button export strain values to a clipboard. These values are only given section-wise, and the values in each sector corresponds to the mean value of the pixels in the sector. The sectors are divided according to American Heart Associations 17-segments model.

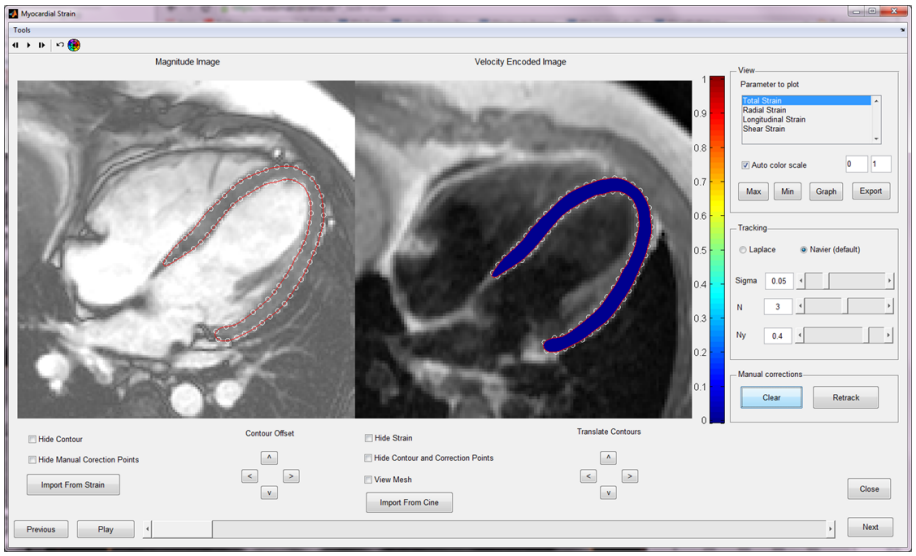


Figure 58: Example of the strain GUI.

34.1.2 Corrections of the segmentation

To make manual corrections in the calculated segmentation select use left mouse click in the image to move contour points. Delete manual point by right click on the added point. When you are satisfied with the manual correction in all time frames push the Retrack button. The Delete button deletes all manual corrections.

34.1.3 Strain analysis

One method to evaluate the strain calculation is to export the segmentation from the velocity encoded image stack to the SSFP image stack after the strain calculation is done. This is done with the button Import From Strain. The motion of the myocardium can then be compared to the myocardial movement in the SSFP image stack. It should be noticed that the two images (SSPF and velocity encoded) are not acquired during the same heart beat which can result in differences in position of the myocardium.

With strain calculated in the current velocity encoded image stack it is possible to produce a graph over time for strain by the button Graph.

In a file that consist of velocity encoded image stacks with calculated strain in all the three long-axis views it is possibly, by clicking the icon of a bullseye plot to produce a bullseye plot of strain.

The function Export From Multiple .mat Files under the menu Strain From Velocity Encoded Imaging under the Strain menu export strain values to clipboard in all `.mat` files in the selected folder.

34.2 Tagging Imaging

The strain tagging analysis module uses tagging MR images to calculate myocardial strain. The module has been developed in close collaboration with researchers at KU Leuven in Belgium.

34.2.1 Automatic strain analysis

1. The automatic strain analysis starts upon loading a tagged image stack. Segment identifies a tagged image stack according to the DICOM tag Series Description. The associated Series Description names can be customized by the user according to Section 11.

2. The strain analysis starts by cropping and upsampling of the image stack, if needed, as shown in Figure 59.

3. The automatic strain registration is then performed in the background. The progress is shown in a progressbar at the bottom of the main interface of Segment. During the registration process the user can perform LV segementation and open the strain analysis interface. The LV segmentation should be performed in the first time frame (or within + 7 time frames from first time frame) in the tagged or potential cine image stack. This time frame will be the initial time frame for the strain tracking.

4. Start the strain module by selecting Strain Analysis under menu Strain From Tagging in the main menu. The Strain interface is shown (Figure 60).

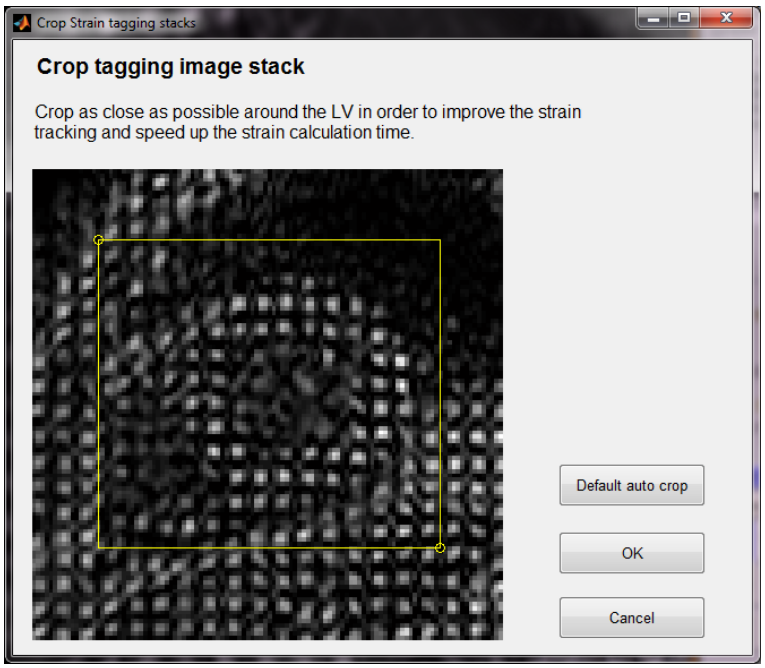

Crop Strain tagging stacks
Crop tagging image stack
Crop as close as possible around the LV in order to improve the strain tracking and speed up the strain calculation time.
Default auto crop
OK
Cancel

Figure 59: Strain cropping interface.

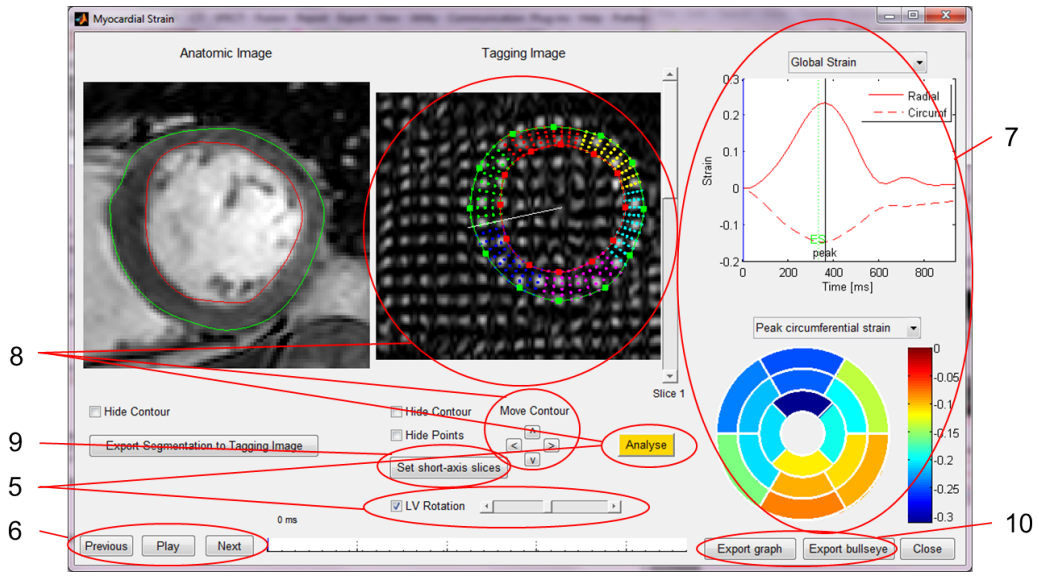


Figure 60: Strain analysis GUI.

5. Define LV rotation by setting the white line in the middle of the RV lumen, using the slider, and press Analyse to run the myocardial strain quantification.

6. Verify the strain tracking by using the movie tools.

7. Strain over time and peak strain is shown in the figures to the right according to the selected parameters.

8. If needed, manual correction can be performed by using the `Move Contour` arrows or moving the LV segmentation interpolation points, in the initial time frame in the tagging image stack. Then run the strain quantification again by select Analyse.

9. Manually change the short-axis slices for the bullseye division by select Set short-axis slices.

10. Click on export buttons to export result to spreadsheet.

35 Image Fusion Module

The functions described in this chapter is in US only for off label use and for investigational use.

Details of this Fusion Module is given in Ugander et al [18].

The image fusion tool is used to compare and fuse one anatomical and one functional image stack. Currently the tool is restricted to rigid body translation and rotation.

An example of the fusion GUI is shown Figure 61. The leftmost panel is the anatomical image stack, the middle the functional image stack and the rightmost the fusion image stack.

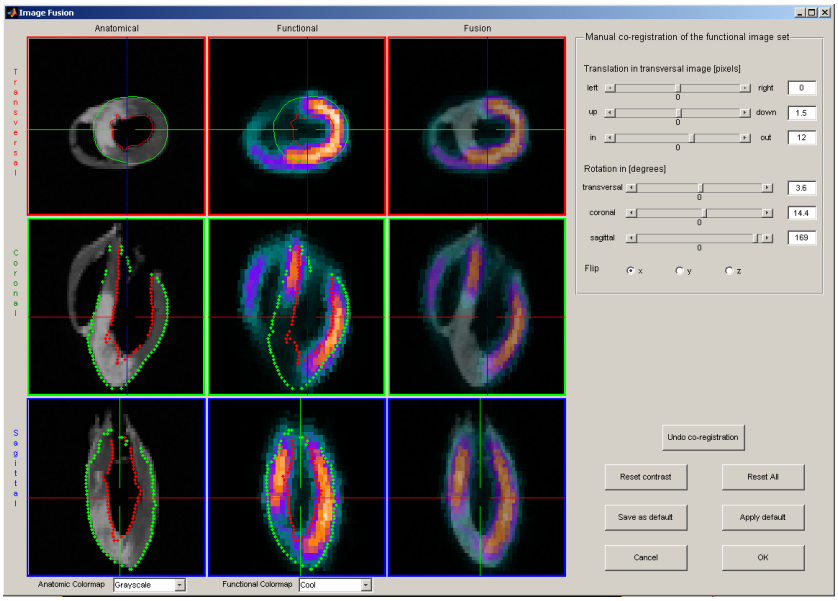


Figure 61: Example of the image fusion GUI.

To start the fusion tool select Fusion of Two Image Stacks under the Fusion menu. You will then be prompted for which anatomical and functional image stacks to fuse. You select by entering a number that are the same as the

thumbnail order (from left) in the main Segment GUI. If the anatomical image stack contains a segmentation this will be shown both in the anatomical and the functional image stack.

Below each image stack the user can manually select color map. The two selections are gray and cool and can be different for the two image stacks. To change the transparency in the fusion image stack hold the right mouse button down and move up or down. In the anatomical and functional image stack the right mouse button will change the brightness (up/down) and contrast (right/left). Click on the left mouse button define the current slice in the image stack. Same slices are always shown in anatomical and functional image stack. The arrow buttons on the desktop can then be used to step in the slices in the last clicked image. If the last click was in one of the co-registration sliders the arrow key buttons will change the position of the slider.

The manually co-registration of the functional image stack is done by changing the parameters in the right box in the GUI. The three sliders and editboxes on the top translate the image stack. The sliders and editboxes in the middle make a rotation in the image stack. The three radiobuttons below the sliders flip the image stack in x- y- and z-direction, respectively.

The Undo co-registration button undoes the last translation or rotation. It also undo the Reset all button. This button reset both co-registrations, colormaps, current slices, contrast and brightness in all image stack to the start values. The Reset contrast button only reset contrast and brightness in the anatomical and functional image stack, and the transparently in the fusional image stack to initial values.

If you need to fuse many data-sets with approximately the same parameter settings, the default buttons can be helpful. The Save as default button saves the current translation, rotation, flip and colormap choices. These settings are then available to use on another data-set. The settings are applied to the image stack by using the button Apply default.

When you are satisfied with the fusion use the Ok button. This results in a new image stack with image type "Fused" and contains the functional images

stack, with the anatomical image stack size, and the segmentation from the anatomical image stack. Example of such an image stack are shown in Figure 62. The parameter settings are also saved and the fusion GUI with the old parameter choices can be open again by select Fusion of Two Image Stacks under the Fusion menu when having an image with image type "Fused" selected. When an image stack with another type than "Fused" is selected, a new fusion GUI always open. Pushing the Ok button in the fusion GUI always result in a new fused image stack.

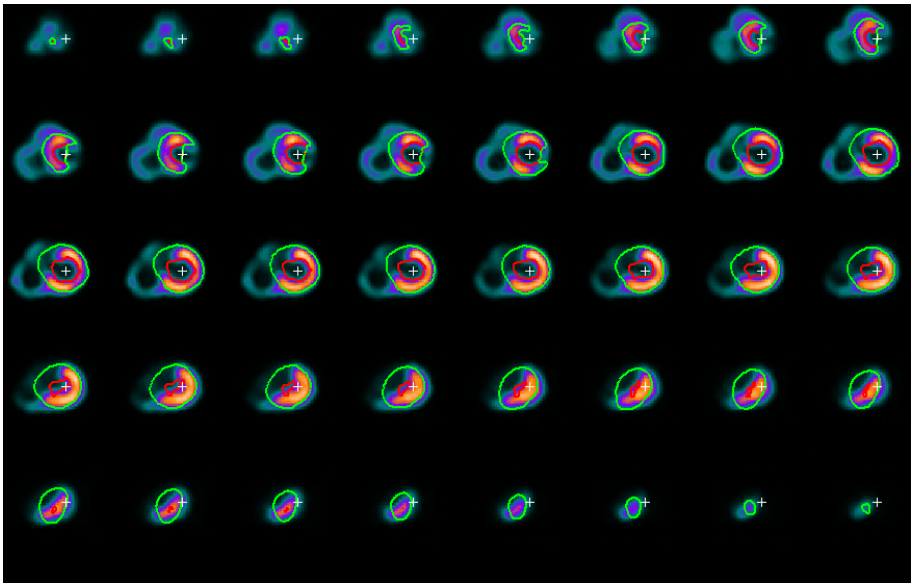


Figure 62: Example of a fused image stack.

36 Perfusion Analysis

The functions described in this chapter is in US only for off label use and for investigational use.

The perfusion module is used for performing analysis of perfusion image stacks. Quotes between maximum upslopes of rest and stress images can be calculated for each sector of the myocardium.

36.1 Module overview

Before opening the perfusion analysis GUI, make sure to have one open image stack whose image type is set to Perfusion Rest and one whose image type is set to Perfusion Stress. An overview of the perfusion analysis GUI, as it appears when launched, is shown in Figure 63. From left to right, each image column contains Stress, Rest, Cine and LGE images respectively. Image slices are shown with the most basal at the top and the most apical at the bottom. If the perfusion stacks contain more than three slices, a scrollbar allows the user to toggle between them. Segmentation contours are shown, but can be disabled by unchecking the ☒ Contour box. The ☒ Rotate checkbox is used to set images in rotation mode. This causes the images to zoom in on the contour, and displays the borders for myocardial sectors as well as a horizontal yellow line from the center to the left of each image. By dragging this yellow line, the user can rotate the images to align them properly with the sector partition. When the mouse button is released, the line will rotate back to its original leftward position and drag the image with it.

The timebars below the Stress, Rest and Cine images enable the user to step in time. The Stress and Rest timebars each have one bar labelled Start and one labelled End. These are used to set the start and end points of motion correction. They also affect use of the playback functionality, which can be done one image at a time using the playback panel with buttons , and , or making Stress and Rest images play synchronously by using the Play all button.

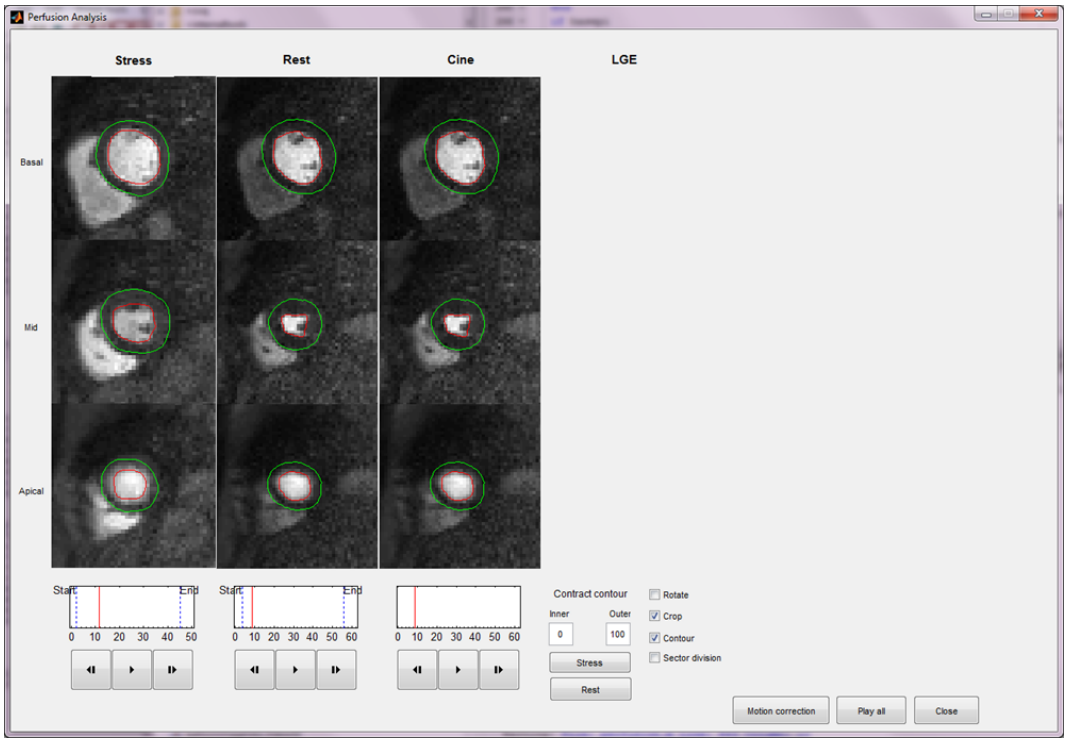


Figure 63: GUI for perfusion analysis.

Once an interval has been set using the Start and End bars and all slices of one timeframe have been outlined in both Stress and Rest image stacks, hit the Motion correction button to start the automatic motion correction. This process can take several minutes. The result is shown in Figure 64. If intensity from the right ventricle or elsewhere spills into the myocardium segmentation as a result of the motion correction, the contour of the respective image stack can be adjusted contraction percentages in the Inner and Outer textboxes and using the Contract Contour pushbuttons labelled Stress and Rest.

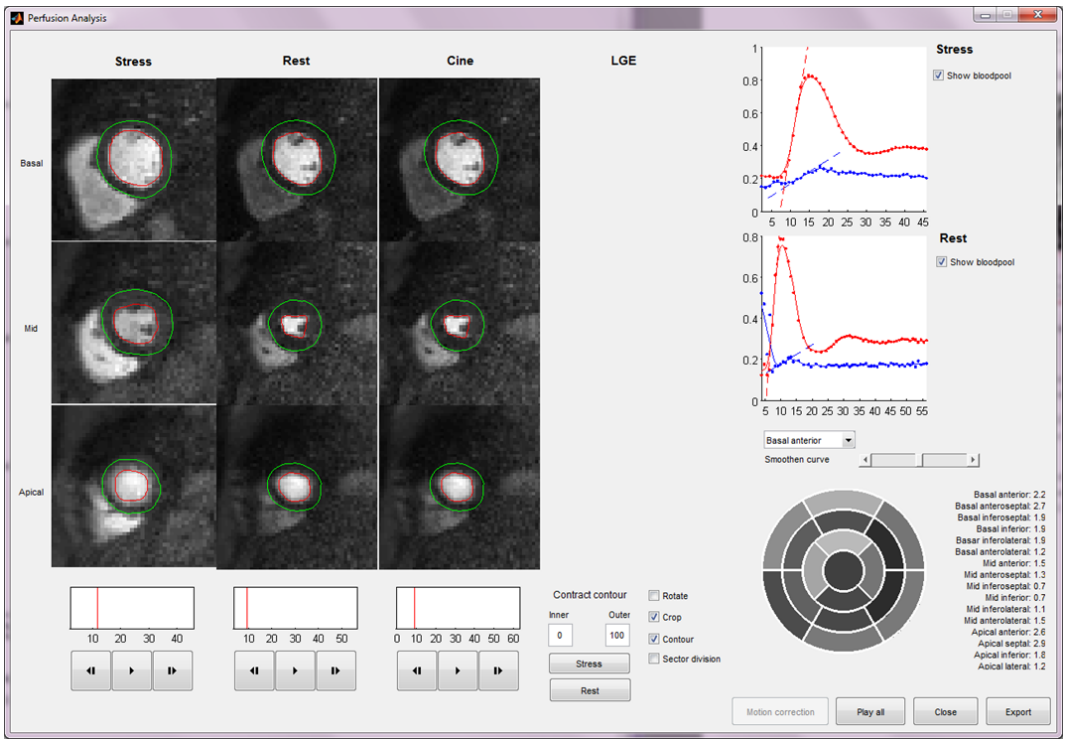


Figure 64: GUI for perfusion analysis after motion correction.

The two plots on the right side of the GUI show the upslope curves of the current sector (selected from the pop-up menu), which are calculated using a Gaussian filter on the measured values. The width of this filter can be adjusted using the slider labelled Smoothen curve, making the curve sharper or smoother. By checking the box ☒ Show bloodpool, a curve of the blood-

pool is shown in red in the same plot. The bullseye plot below the curve plots displays the sectorwise quote between the maximum stress and rest upslopes, normalized with respect to the respective maximum upslopes of the bloodpool curves. The quote values are also shown in text next to the bullseye plot, and can be exported to a spreadsheet by clicking the Export button.

37 Native Bruker Reader Module

The functions described in this chapter is in US only for off label use and for investigational use.

This module to load native Bruker files is a commercially available module to Segment. The structure (files and directory) of the Bruker Paravision file format is given in the Imaging Wiki:

`http://imaging.mrc-cbu.cam.ac.uk/imaging/FormatBruker`

Some further details in the file format used in the Bruker Module is given in Section 37.1.

The reader is available under the File menu. The file loader GUI is shown in Figure 65.

The first step is to select the subject file. This file is usually called just `subject` or `subject.txt`. Then all available subject info is shown in the top left panel. A list of available studies are shown in the lower left panel. When selecting on study the image series (usually only one) are displayed. The Load will load the selected studies/series. To load many studies into one image stack, just select more studies in the lower left panel. Note that when loading many studies into one image stack each study needs to contain only one image serie.

The button Dismiss will close the file loader. The button Clear will clear the current subject to allow you to select another subject.

The following limitations apply to the Bruker reader:

- The reader is still experimental and all paravision features may not be implemented. If you are experience problems with the Bruker reader, please report them to `support medviso.com`.

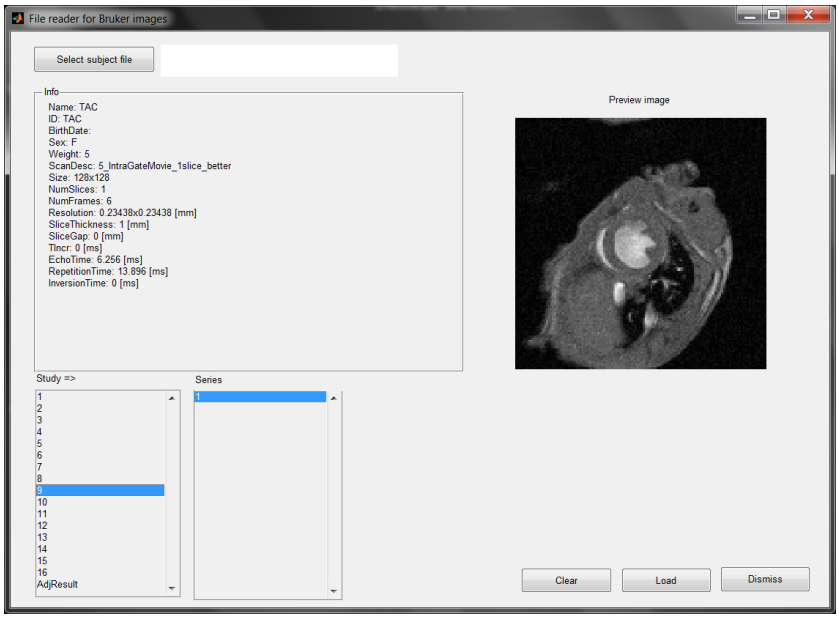


Figure 65: File GUI for loading bruker images.

- The reader does currently not read 3D coordinates, and thus the plane intersection features in Segment will not work.
- The reader does not read phase contrast images. Please let us know if this is a desired feature. We will need to have some example images since we do not have access to details about this.
- Timing (time increment between frames) may not be correctly calculated unless for IntraGate scanners. Timing information is taken from `EchoTime` and `RepetitionTime`, please see Section 37.1.7 for details.

37.1 Implementation details

In this section details on how Segment interprets the Bruker File format is given. An overview of the folder tree for a Bruker examination is given in Figure 66. This example examination contains two scans and where the first scan contains two series.

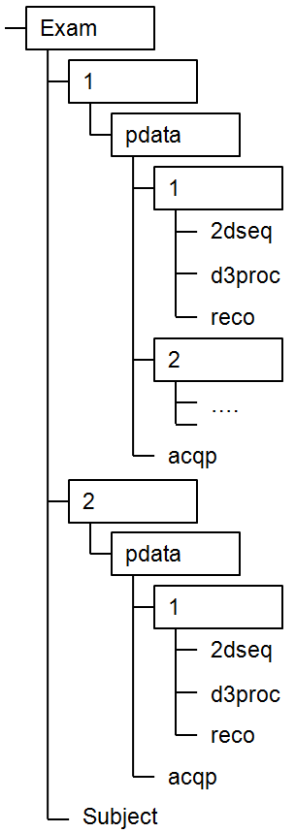


Figure 66: Example of file/folder tree for a Bruker examination. In this case the number of scans are two, and for scan 1 there are two series. Boxes represent folders and plain text without a box represent a file. Only the illustrated folders and files are read, all other files and folders are ignored.

37.1.1 Read files

The following files are read by the Bruker reader module (all other files are ignored):

- `subject` file. This file contains subject data common for the entire exam.
- `acqp` file. This file contains image acquisition information of the scan.
- `reco` file. This file contains information for the image serie.
- `d3proc` file. This file contains additional information for the image serie.
- `2dseq` file. This file contains the image data for each image serie.

Each file may have the optional ending `.txt`.

37.1.2 Parsing the `subject` file

The first step of loading Bruker files is to select a subject file. The following parameters are read from the subject file:

- `$SUBJECT_id` is parsed to Patient ID.
- `$SUBJECT_name_string` is parsed to Patient Name.
- `$SUBJECT_dbirth` is parsed to Patient Birth Date.
- `$SUBJECT_sex` is parsed to Patient Sex. Here the string `female` (not case sensitive) is mapped to `F` and male is mapped to `M`. All other strings are mapped to `-`.
- The patient age is not read from the subject file and is set to empty. Reason for not reading that is that we have not found files containing this information.

37.1.3 Parsing `acqp` file

The following data is read from this file:

- `$ACQ_spatial_size`, from this vector the two first elements are taken as `YSize` and `XSize`, respectively.
- `$ACQ_flip_angle` gives `FlipAngle`.

- $ACQ_slice_thick gives SliceThickness. Please note that this information is read as safe guard if the other files are missing. This value will be overwritten in most cases.
- $ACQ_echo_time give EchoTime.
- $ACQ_repetition_time give RepetitionTime.
- $ACQ_trigger_delay give TriggerDelay.
- $ACQ_n_movie_frames give the number of timeframes (TSize). Please not that is read as safe guard if the other files are missing. This value will be overwritten in most cases.
- $NSLICES gives the number of slices. Please not that is read as safe guard if the other files are missing. This value will be overwritten in most cases.
- $ACQ_slice_orient gives ImageViewPlane.
- $ACQ_inversion_time gives InversionTime.
- $ACQ_scan_name gives SeriesDescription.
- $ACQ_method gives ImagingTechnique.

37.1.4 Parsing reco file

The following elements are read from the reco file:

- $RECO_size gives the reconstruction size of the image (YSize,XSize), and if there are multiple slices also ZSize. If this vector only contains two elements, then ZSize is taken as the number of elements in the $RECO_transposition, otherwise it is taken as the third element of $RECO_size.
- From the element $RECO_fov the pixel size is taken. If this element contains three number then this information is divided with the number of slices to get SliceThickness.
- The number of images is extracted from the number of items in element $RECO_globex. From this the number of time frames TSize is calculated a number of images divided by the number of slices. If this is not a valid number of time frames, then the number of frames is set to 1. Please note that this information is updated when reading the d3proc file.

- The bit depth of the `2dseq` file is taken from the element `$RECO_wordtype`.

37.1.5 Parsing `d3proc` file

The following elements are read from the `d3proc` file:

- `$IM_SIX` gives `YSize`.
- `$IM_SIY` gives `XSize`.
- From the element `$IM_SIZ` and `$IM_SIT` a temporarily zsize and tsize are extracted. If this information does not match the previously extracted information for number of slices and number of timeframes, then the number of timeframes are calculated as zsize divided by the previously extracted number of slices (from the `reco` file). If the newly calculated number is not a valid number of timeframes, then the number of timeframes is taken from tsize.

37.1.6 Parsing `IntraGate.info` file

Depending on if the scanner is an IntraGate Bruker scanner, this file may exist. If it is existing, then the following information is read from the file:

- `par::heartrate` this element gives the heart rate of the subject (`HeartRate`).
- `par::heartsignalDuration` this element is combined with `par::heartframes` to get the time increment between each timeframe (`TIncr`).
- `par::heartframes` is checked against number of previously detected timeframes and an error is issued if there is a mismatch.

37.1.7 Reading timing information

Unless for the IntraGate scanner, the timing information (time increment between timeframes, `TIncr`) is taken as the repetition time (if present), and otherwise, taken as the echo time.

38 Report Module

This functionality is only available in the clinical/commercial version of Segment.

The report tool is a report generator is a tool to generate reports of a study. The tool is started by the icon or under the Report menu. The graphical user interface is illustrated in Figure 67. The report can be generated in one of three formats:

- HTML format. The Generate HTML report is used to generate a HTML report, complete with images and plots. Each page can be printed and together they contain a detailed report of an exam. An example of the final output is given in Figure 68.
- JPEG format. A simplified graphic report, containing only text and tables, can be created using the Send to PAF button. This report is saved as a collection of JPEG files for easy upload to PAF. The output folder can be set in the Advanced System and DICOM settings under the Preferences menu.
- DICOM format. The simplified graphic report can also be saved as a collection of DICOM files and automatically uploaded to PACS by clicking the Save to PACS button.

Hospital logo, patient data, signature field and current date are automatically included in the report. The checkboxes are used to select which details of the analysis are to be included in the report. A checkbox is grayed out if data is unavailable.

- LV Analysis, this section contains a table of global LV parameters and, if the images are time-resolved, a volume curve.
- RV Analysis, this section contains a table of global RV parameters.
- Scar Analysis, this section contains a table of data from scar analysis and an image of scar delineation.
- MaR Analysis, this section contains a table of data from myocardium at risk analysis.

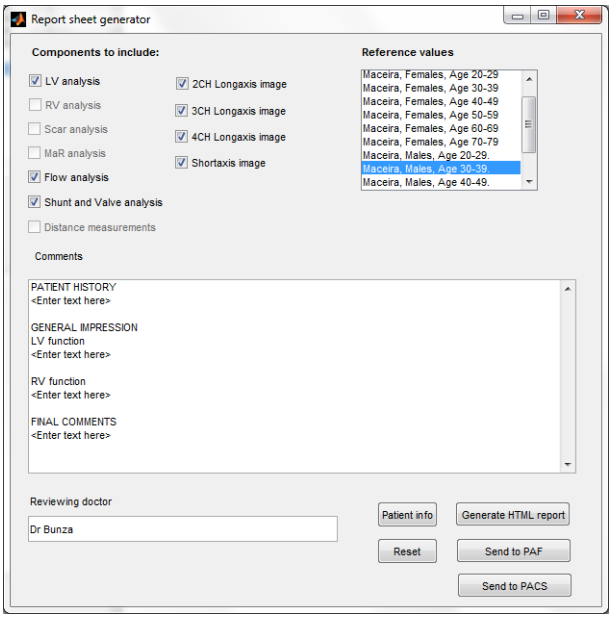


Figure 67: GUI for patient report generator.

- Flow Analysis, this section contains flow data from phase contrast images and a plot of net flow over time. If there are several image stacks containing different flow data, one section will be added for each such stack.
- Shunt and Valve analysis, this section contains the Qp/Qs ratio and regurgitant volumes and fractions for the mitralis and tricusp, insofar as the data necessary for calculation is available.
- Distance measurements, this section contains a table that lists all distance measurements performed on the current set of image stacks.
- 2CH/3CH/4CH Longaxis Image, this section contains a user selection of longaxis images in end-diastole.
- Shortaxis Image, this section contains a montage view of all shortaxis image slices in end-diastole with delineations included.

38.1 Configuration

This section describes how the Report Module can be configured.

38.1.1 Hospital logo

This is an image header that is supplied by Medviso AB to each customer separately. Place this file in the folder where Segment is installed.

38.1.2 Reference values

Reference data used in LV and RV analysis can be selected from a listbox. If patient age and sex are present in the patient info, the listbox will automatically suggest a suitable set of reference values. If reference data is used in the report, patient values outside the range specified by the reference data will be marked in red. The name of the used reference data set will also be included in the report.

A directory contains each reference data set as a text file with the following structure:

```
Name:  'Maceira, Males, Age 30-39.'  %Title to display in listbox.
ImagingType:  'SSFP' %Describes used imaging type.
LowerAgeBound:  30
UpperAgeBound:  39
Sex:  'M' %should be either M or F.
LVM: [109 185]
EDV: [121 204] %range
...
EDV_BSA: [66 101] %_BSA means normalized with BSA.
...
```

38.1.3 Headings for textual report

There is also a large textbox where it is possible to enter free text comments on the study. This text is then stored together with the segmentation. A few formatting tricks can be used in this box:

- To divide the text into paragraphs, enter a blank line between the text blocks to be used as paragraphs.
- To start a paragraph with a headline in bold print, simply begin the paragraph with the text to be used as headline, then insert a new line where the text body is entered.

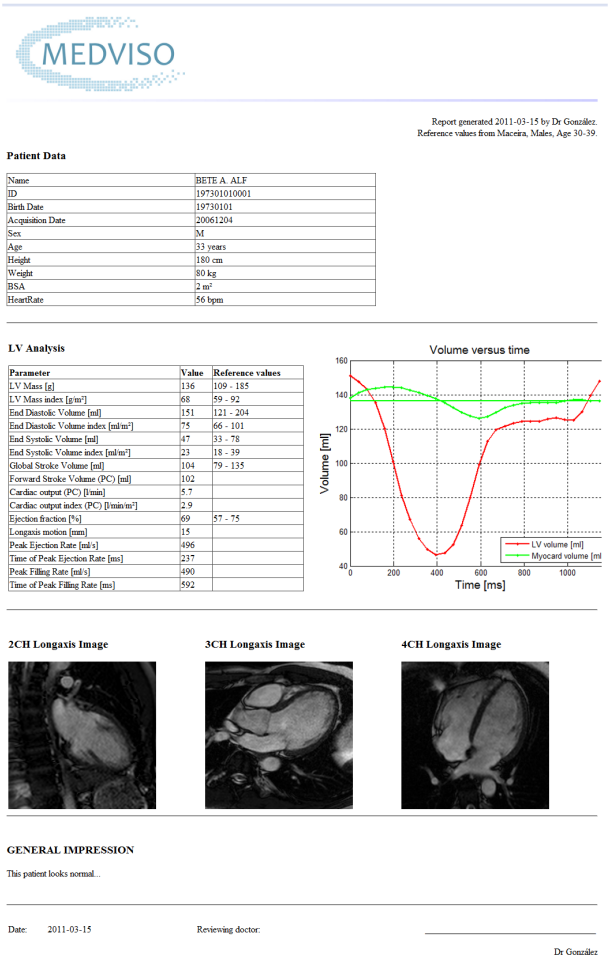
- To insert a super headline, do the same as above except that the text is entered in all upper-case letters. A super headline may be followed by a regular headline.

For simplification, standard text templates are supplied by Medviso AB. An example of such a template is the following:

```
PATIENT HISTORY
<Enter text here>

GENERAL IMPRESSION
LV function
<Enter text here>

RV function
<Enter text here>

FINAL COMMENTS
<Enter text here>
```

38.1.4 Reviewing doctor

The final textbox in the GUI allows for including the name of the doctor performing the analysis and generating the report. If entered, the name of the doctor appears by the logo image at the beginning and by the signature field at the end of the report.



MEDVISO

Report generated 2011-03-15 by Dr González.
Reference values from Maceira, Males, Age 30-39.

Patient Data

Name	BETE A. ALF
ID	197301010001
Birth Date	19730101
Acquisition Date	20061204
Sex	M
Age	33 years
Height	180 cm
Weight	80 kg
BSA	2 m²
HeartRate	56 bpm

LV Analysis

Parameter	Value	Reference values
LV Mass [g]	136	109 - 185
LV Mass index [g/m²]	68	59 - 92
End Diastolic Volume [ml]	151	121 - 204
End Diastolic Volume index [ml/m²]	75	66 - 101
End Systolic Volume [ml]	47	33 - 78
End Systolic Volume index [ml/m²]	23	18 - 39
Global Stroke Volume [ml]	104	79 - 135
Forward Stroke Volume (PC) [ml]	102	
Cardiac output (PC) [l/min]	5.7	
Cardiac output index (PC) [l/min/m²]	2.9	
Ejection fraction [%]	69	57 - 75
Longaxis motion [mm]	15	
Peak Ejection Rate [ml/s]	496	
Time of Peak Ejection Rate [ms]	237	
Peak Filling Rate [ml/s]	490	
Time of Peak Filling Rate [ms]	592	

2CH Longaxis Image

3CH Longaxis Image

4CH Longaxis Image

GENERAL IMPRESSION

This patient looks normal...

Date: 2011-03-15 Reviewing doctor:

Dr González

Figure 68: Example of a report.

39 Short Commands / Hot keys

This chapter describes the hot keys that can be used in the program. Note that in many places you can also bring up a pop-up menu by using the right mouse key to more easily access frequent menu items.

39.1 Hot keys

`D`	Go to end diastole
`S`	Go to end systole
`Shift-D`	Go to end diastole in all visible image stacks
`Shift-S`	Go to end systole in all visible image stacks
`Left arrow`	Previous time frame
`Right arrow`	Next time frame
`Up arrow`	Next slice in basal direction
`Down arrow`	Previous slice in basal direction
`Shift-Arrows`	Same ass Arrows but applies to all visble image stacks
`C`	Start to play cine thumbnail
`P`	Start to play movie
`Shift-P`	Start to play movie of all visible image stacks
`R`	Refresh screen
`H`	Hide/show all contours and markers
`V`	Shift mode in panel between montage and one slice
`Ctrl-A`	Selects all slices
`Shift-U`	Unselect all slices
`Shift-A`	View all image stacks
`Shift-1`	View one image panel
`Shift-2`	View two image panels
`Alt-2`	View two image panels as rows
`Shift-3`	View three image panels
`Alt-3`	View three image panels as rows
`Shift-4`	View three image panels
`Shift-6`	View six image panels
`Alt-6`	View six image panels as rows
`Shift-9`	View nine image panels

Ctrl-1	One view
Ctrl-2	M-mode view
Ctrl-3	Montage view
Ctrl-4	Montage row view
Ctrl-5	Montage fit view
Ctrl-L	Perform fully automatic LV segmentation
Ctrl-M	Segment LV endocardium
Ctrl-Shift-M	Segment LV epicardium
Ctrl-Alt-M	Segment RV endocardium
Ctrl-R	Refine LV endocardium
Ctrl-Shift-R	Refine LV epicardium
Ctrl-Alt-R	Refine RV endocardium
Alt-R	Refine Flow ROI
Ctrl-F	Propagate LV endocardium (epi if next timeframe already has er
Ctrl-Shift-F	Propagate LV endo and epicardium forward and refine
Ctrl-Alt-F	Propagata RV endocardium forward, do not refine
Alt-F	Propagate Flow ROI forward and refine
Ctrl-T	Track tool for LV endocardium
Alt-T	Track tool for Flow ROI
Ctrl-U	Copy LV endocardium upwards and refine
Ctrl-Shift-U	Copy LV epicardium upwards and refine
Ctrl-Alt-U	Copy RV endocardium upwards and refine
Ctrl-D	Copy LV endocardium downwards and refine
Ctrl-Shift-D	Copy LV epicardium downwards and refine
Ctrl-Alt-D	Copy RV endocardium downwards and refine
Ctrl-V	Exclude papillary muscle from LV enocardium
Space	Toggle tool in toolbar menu (depending on tool and mode).
Shift-L	Select LV mode
Shift-R	Select RV mode
Shift-F	Select ROI/Flow mode
Shift-V	Select Scar(Viability) mode
Shift-M	Select MaR mode
Shift-I	Select Misc mode
Ctrl-B	Bullseye plot
Ctrl-N	Load next .mat file
Ctrl-O	Load image stack
Ctrl-P	Open patient data base
Ctrl-Shift-G	

¿ Reset GUI Position

`Ctrl-S`	Save all image stacks
`Ctrl-W`	Close current image stack
`Shift-Ctrl-W`	Close all image stacks
`Ctrl-Q`	Quit program
`Ctrl-Z`	Undo segmentation
`Ctrl-plus`	Zoom in
`Ctrl-minus`	Zoom out
`Mouse wheel`	Scroll through slices
`Shift-Mouse wheel`	Scroll through time frames
`Ctrl-Mouse wheel`	Scroll through visible thumbnails
`Alt-Mouse wheel`	Zoom

40 How to Reference the Software

To be permitted to use the software for research purposes you need to reference the usage of the software properly, for more details see Chapter 2. This is very important since it is necessary that we can prove to granting organisations that this project returns scientific output and has a significant impact to the scientific community.

A reference should encompass both the name and version of the software, and a reference to a suitable scientific publication about that function in Segment. It should also be indicated that the software is free for research purposes, and the address homepage of the software (`http://segment.heiberg.se`).

You should reference the software differently depending on what part of the software that have been used. This list is subject to change after submitted papers are accepted. *Always* check the homepage for the latest information regarding this issue. In doubt please do not hesitate to contact the author, or place the generic Segment reference [19].

Note that referencing the software is mandatory also for abstracts to scientific conferences. It shortage of space, reference the software as something like:

... Images was analyzed using the freely available software Segment (`http://segment.heiberg.se`).

In extreme shortage of space, such as conferences where the word limit is < 350 words then reference may be omitted in the abstract text, but should be included in the oral presentation and / or poster.

The following list describes various usage of Segment and how it should be referenced.

- General usage of Segment should be reference [19]. This reference is the generic reference for the Segment project.

- Automated and manual delineation of the left ventricle on MRI images to get LV volume, ejection fraction, etc, should be referenced as [20] or [21], or preferable [19].
- Automated quantification of infarct size and transmurality should be referenced as [5] or [4] depending on what mode have been used. If weighted mode have been used to quantify infarct transmurality, then paper [22] should be used.
- Flow quantification should be referred to as [19].
- Strain analysis should be referred to as [16].
- Segmentation of the left ventricle in non gated SPECT images should be referenced to as [23].
- Segmentation of defect size of myocardial at risk from SPECT images should be referenced to as [24].
- Segmentation of myocardium at risk from T2 STIR imaging should be referred to as [9].
- Segmentation of myocardium at risk from cine delayed enhancement should be referenced to as [25].
- Measurement of endocardial extent should be referenced to as [26].
- Creating polar plots should be referred to as [27].
- Fusion data sets should be referred to as [18].

40.1 Examples of possible formulations

- *... left ventricular mass and ejection fraction was measured using Segment v2.0 R4790 (`http://segment.heiberg.se`) [21].*
- *... Infarct size were determined using Segment v2.0 R4790 (`http://segment.heiberg.se`) [5].*
- *... Image analysis was performed using the freely available software Segmentv2.0 R4790 (`http://segment.heiberg.se`) [19].*

41 Support

The commercial license of Segment includes technical support by email. It also includes simple feature request such as specialized output formats. Furthermore a commercial licensee will be given a significant weight on how a bug report is prioritized. Bugs reported by users of commercial license are usually fixed within 1-2 days. The support is provided by Medviso AB.

With this said, we encourage all users to come with questions and feedback, but we do not guarantee that we will have time to answer your questions.

41.1 Submit bug report

When submitting a bug report it is very important to describe how to reproduce the bug and to provide the log file for the session. In many cases it is also necessary to provide some files that can be used to analyse the problem. It may either be `.mat` files or DICOM files when the problem is loading data into Segment.

To submit a bug report, select the function Support Request under the Help - Support menu. This will open the graphical user interface where you can describe the bug and attach log files and data such as `.mat` files or DICOM files. When all information is entered you press the Send support request and the description entered and the attached files are submitted to Medviso.

By changing the type you can also submit general questions or enhancement requests.

Hints to remember:

1. Even though the submitted files are encrypted your files should be anonymized. Anonymization of `.mat` files are available under either Image Tools menu or the Utilities menu. Anonymization of DICOM files are available under the Utilities menu.

2. Additional files to submit should be placed in a folder and the folder is then submitted.

3. Remember to name your files wisely, otherwise we will not be able to identify which file belongs to which support request.

4. Remember to mention the filename uploaded in your support question/request.

41.2 Data privacy policy

Medviso AB will strictly keep the data safe and **not** distribute it and any data or information from it (such as possible pulse-programming ideas, post-processing ideas, etc etc). Medviso will **not** utilize it for other purposes than debugging purposes or to answer the specific questions unless other is agreed upon. When the support case has been closed, then the data will be deleted. If you have questions, please contact `support@medviso.com` for further details.

41.3 General support issues

To get into contact with developers at Medviso AB, send email to `support@medviso.com`.

42 Segment User Community

As a result of the growing interest in Segment and as a response of numerous requests Medviso AB has started to form a user community web place. This initiative will be enlarged significantly as the members of the community both requests more and also expands the community. It is worth noting that in the user survey spring 2010, out of 169 answers 147 answered that they would follow the user community, and 45 answered that they would follow it often.

A preliminary start page of the user community can be found on the following Facebook page `http://www.facebook.com/pages/Segment/119840021370285`.

It is the aim to be able to provide the following activities on the user community pages:

1. Participate in discussion forums. Currently forums for Developers discussion and tips and tricks, Feature requests, Segment and Mac.

2. Contribute and share own plug-ins. This feature is currently not available. If you have plug-ins that you want to share, please email them to `support@medviso.com` and we will manually upload the plug-in. Currently writing own plug-ins to Segment is documented in the Segment Technical Manual.

3. FAQ sections. Currently we are gathering FAQ in our support program. All (or almost all) support request will be made available in a searchable data base. Exceptions on when support requests are not included when the user request so in conjunction with classified projects.

Staff from Medviso AB will follow the user community page closely and monitor any incoming questions or uprising discussions.

If you have any ideas or suggestions on how we should improve the user community, please send us an email to `support@medviso.com`.

43 Plugins

The functions described in this chapter is in US only for off label use and for investigational use.

In Segment it is possible to create own plugins and extensions. This is further described in [19] and the Technical Manual. Currently there are two plugins that are shipped with the stand-alone version of Segment.

43.1 Image Loader Plugin

The image loader plugin is used to load diffrent kinds of images into segment. The plugin currently supports the following image formats.

- JPEG (*.jpg)
- PNG (*.png)
- TIFF (*.tif)

There are two diffrent ways of loading images in the image loader plugin. The first way, called Load single file, load a single image file in a new image stack. The second way, called Load files from directory, loads all files in a directory and places them in a single image stack. The images are ordered according to filename and placed in z-depth.

Some information, such as resolution, that exist in dicom files are not present in these general image formats. The image loader plugin will simply guess on default values for these values. Sometimes one can use the calibrate plugin to set the resolution to a correct value.

43.2 Image Calibration Plugin

Sometimes the correct resolution for an image stack isn't known. However if one knows the area of some region of the image beforehand one can calculate the correct resolution. This plugin helps one do that.

When loading the plugin one is presented with a red square. By moving the corners of the square one can select the region. One is also presented with a input box where it's possible to enter the area of this region. When

pressing the ok button the plugin calculate the correct resolution and updates the image stack accordingly. Note that this plugin assumes isotrope images.

44 Implementation Details

In this chapter a few implementation details are given. There are much more details that are interesting, but this is as far as we have got with the documentation. If you have specific questions, please do not hesitate to ask us.

44.1 Version handling

A proper version handling is employed when developing Segment. A detailed version history of Segment is found in the revision log of Segment SVN.

44.2 Numeric representations

All numbers are stored and used internally as double precision floating points with the following exceptions:

- Images are stored as single floats (normalized) or as integers (uint8), and then as they are stored in the DICOM files. Most functions in Segment will automatically convert the data to floats.
- Edge detection results are stored as integers (16 bits, 'normalized')
- Character strings are stored in 8bit ASCII format
- Infarct maps are stored as int8 (manual interaction), and uint8 (result).
- General segmentation tool store objects as levelset function with an uint8 representation where the zero levelset resides at 128.

Internally the image stack is normalized upon loading by a global maximum intensity such that all values are [0..1]. Offset and scaling is also calculated so that the image stack can be reconverted back to original signal intensities.

44.3 Loading data and interpretation of DICOM tags

This section describes how Segment interprets DICOM information to calculate important parameters suchs as geometric properties of the images.

- Number of slices. This is calculated from the presence of different slices based on the DICOM tags `ImagePosition` and `ImageOrientation`.
- Number of timeframes. This is based on dividing the total number of images with the number of slices.
- Time increment in ms between each timeframe. If uniform, this is based on the difference between the number of timeframes divided by largest and the smallest value of the DICOM tag `TriggerTime`. If the DICOM tag `TriggerTime` is not present then the DICOM tag `TR` is used as time increment. Note that this might depent on your k-space acquisition scheme so for scanners that do not report `TriggerTime` you really need to double check the estimated value of time increment. For perfusion and other image stacks with non-uniform time increment, this is calculated using differences in `AcquisitionTime`.
- Heart rate. The heart rate is taken from the DICOM tag `HeartRate` if present. Note that many vendors (including Siemens) does not specify this. As a fall back Segment tries to calculate the heart rate assuming full R-R intervall coverage by using of trigger time (i.e it does not working for prospective imaging series). For long image acquisitions where one image is taken approximately for each heart beat then the heart rate is taken as the time between start of image acquisition and end of image acquisition adjusted for the number of frames. Note that in many cases this heart rate calculation will fail. Heart rate can be adjusted under patient details. Note also that heart rate may vary between image stacks therefore do not press Apply for all when manually changing heart rate. Heart rate is not used in any calculaion, instead time increment between image frames is used in all calculations.
- Slice thickness in mm. The slice thickness is taken from the DICOM tag `SliceThickness`. If this tag is not present then the information is taken from same DICOM tags as number of slices, and assuming slice gap to be 0.
- Gap between slices in mm. This is taken from the DICOM tag `Spacing BetweenSlices`.
- Pixelspacing in X-direction in mm (vertical direction in Segment). This is taken from the DICOM tag `PixelSpacing`.
- Pixelspacing in X-direction in mm (horisontal direction in Segment). This is taken from the DICOM tag `PixelSpacing`.

- Velocity encoding (VENC) in cm/s. For non velocity encoded images this should be 0. How this is interpretated involvs proprietry information of different scanner vender information.
- Rotated image stack. This should by default be false. If your image stack is rotated, then change this to true. Currently this parameter is not taken from information in the DICOM tags and the user needs to manually change this when loading rotated image stacks.
- Cyclic image. If the image stack is cyclic, i.e covers the whole heart cycle this should be true (default). For prospectively gated image series this should be false. This affects mainly the automated segmentatin algorithm. Currently this information is not read from the DICOM information.

44.4 Volume calculations

The volume calculations are done by a summing the area in each slice. The main reason for not using a more advanced volume integration method is that no one else is using that and therefore it might be difficult to compare the results. Segmentation (i.e. delineation of endocardium and epicardium) is stored on a sub-pixel accuracy and subsequent calculations are on a sub-pixel basis. For viability the classification into viable or scar is done on a pixel-wise basis and there the volume calculations are done by summing the number of pixels.

For the rotated image stacks the volume is given by a integration method. The volume contribution of each outline is given by :

$$\delta V = \frac{\pi}{2 * Z} \int y(s)^2 \texttt{sign}(y(s)) \frac{dy}{ds} ds \tag{1}$$

where the curve is given on a parametric representation $(x(s), y(s))$, Z is the number of slices in the rotated image stack. No long-axis compensation is performed for the rotated image stacks.

44.5 Mass calculations

When converting volume to mass the density is assumed to be 1.05 g/ml. Note that this number differs in the literature between 1.04 to 1.05. Further-

more, note that these numbers are valid for healthy myocardium ex-vivo, what happens in for instance infarcted regions is not shown in the literature. Therefore usually it is better to report volume instead of mass.

44.6 Calculation of BSA

The formula used is based on Mosteller.

$$BSA = \sqrt{\frac{w * h}{3600}} \tag{2}$$

where w is the body weight in kg, and h is height in cm.

44.7 Peak ejection/filling rate

When calculating peak ejection and peak filling rate the volume curve is differentiated using forward difference approximation. For cyclic datasets cyclic convolution is used for the calculation.

44.8 Wall thickness

Currently wall thickness is defined as the thickness along a radial spike from the endocardial or the epicardial center (depending on setting in the preferences. In the future I plan to also include the modified center line method. Note that the centers are calculated for each timeframe separately.

Wall thickening is defined as the wall thickness in end-systole minus the wall thickness in end-diastole. Note that it is possible to manually or automatically select what timeframes that are diastole or systole respectively.

Fractional wall thickening is defined as:

$$WT_f = \frac{WT - WT_{ED}}{WT_{ED}} \tag{3}$$

Where WT_f is fractional wall thickness and WT is wall thickness and WT_{ED} is wall thickness in end-diastole. In the bulls eye plot then fractional wall thickening is showed in end-systole.

44.9 Calculation of regurgitant volumes and shunts

The regurgitant fraction for the aortic valve and the pulmonary values are calculated as:

$$r = 100\frac{v_{back}}{v_{forward}} \tag{4}$$

where r is regurgitant fraction, v_{back} is backward volume, and v_{forwd} is forward volumes. Backward volumes is taken as timeframes where the net flow is negative and integrated over the entire cardiac cycle.

The regurgitant fraction for the tricuspid and mitral valve are calculated as:

$$r = 100\frac{SV - v_{forwd}}{SV} \tag{5}$$

where r is regurgitant fraction, and SV is stroke volume for left or right ventricle, respectively. v_{forwd} is forward volume.

The Q_p/Q_s ratio is defined as

$$Q_pQ_s = \frac{Q_p}{Q_p} \tag{6}$$

where Q_p is the stroke volume of the pulmonary artery and Q_s is the stroke volume of the aortic artery.

44.10 Infarct size, extent and transmurality

Calculations of infarct sizes etc are based on 'counting' pixels, i.e. each pixel has a binary classification. There are two methods for regional analysis available, one are based where the percentage of the pixels that are inside the sector. The other method is based on radial spikes from the center (endo- or epicardial depending on setting in the preferences). The line between endocardium and epicardium is resampled in 50 steps and the percentage of infarcted pixels are counted.

Infarct extent is defined as the projected infarcted area on the endocardial surface [26].

$$I_{ext} = \sum_i \frac{T_i R_i}{R_i} \tag{7}$$

where I_{ext} is the infarct extent, T_i is the transmurality of sector i and R_i is the mean endocardial radius of sector i.

44.11 Number of SD from remote for Scar

The number of SD from remote for an existing scar segmentation is calculated by the function found in the main menu in Segment under MR menu Viability menu and then the menu option Get SD from Remote. The presented value is calculated by first calculate the mean and sd in the remote area ($Mean_{remote}$ and SD_{remote}). If there exist ROIs named `Remote ROI`, these regions define the remote area. Otherwise the whole myocardium except for the scar region defines the remote area. The presented SD from remote value is then calculated by

$$SDfromRemote = \frac{T_{optim} - Mean_{remote}}{SD_{remote}} \tag{8}$$

The optimal threshold value (T_{optim}) represent the optimal threshold for seperating the remote and the scar regions based on the existing scar segmentation. This value is defined by an exhaustive search where the threshold is set to all intensities represented in the image stack. For each threshold, the number of missclassified pixels are counted (total of both missclassified remote pixels and missclassified scar pixels). The optimal threshold value is then defined as the threshold corresponding to the minimal number of missclassified pixels.

44.12 T2/T2* calculation implementation

The signal intensity S in the images can be described with an exponential fit according to:

$$S = K * e^{(-R_2 \cdot T_E)} \tag{9}$$

where R_2 is $1/T_2$, and K is an arbitrary constant. In order to calculate the exponential fit one need at least three echo times (in theory two would be enough, but to ensure numerical stability Segment requires at least three points in time. The curve fitting is solved by taking the logarithm:

$$\texttt{ln}(S) = -R_2 \cdot T_E + K. \tag{10}$$

where S is the signal intensity of the pixel, R_2 is $1/T_2$, T_E is the echo time, and K is an arbitrary constant. This equation is solved for each pixel withing the region of interest in a least square sense by standard direct numerical method. Finally the T_2 value is calculated as $1/R_2$.

In the litterature, there are some evidence that a constant is advantageous in the fitting process [28]. This constant will be implemented in later versions of the module.

44.12.1 Calculating fitting error

The fitting error is calculated as the error of the reconstructed signal minus the true signal value for each pixel and echo time. The error for each pixel is calculated as the mean of the absolute value of the percentage errors for all echo times.

44.12.2 Smoothing

The smoothing process is done by normalized averaging, where the certainty of each pixel is taken into acount to avoid the effect of uncertain pixels [29].

The smoothing kernel is a Gaussian smoothing kernel, illustrated in Figure 69.
The certainty is calculated linearly as a function of the error measure calculated in Section 44.12.1. Pixels with an error with 25% or more are assigned a certainty of zero, and pixels with zero error are assigned a certainty of one. The cut of value of 25% is taken from [30]. Pixels where the T2/T2* value is negative is also assigned a zero certainty. The normalized averaging is calculated by first calculating a filtered version of the T2/T2* map multiplied with the certainty as:

$$\boldsymbol{M} = (\boldsymbol{T} \cdot \boldsymbol{C}) * \boldsymbol{F} \tag{11}$$

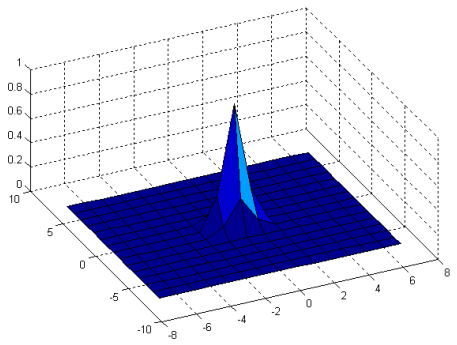


Figure 69: The filter used for smoothing.

where $\boldsymbol{T}$ is the raw T2/T2* map, $\cdot$ is pixelwise multiplication, $*$ denotes convolution, $\boldsymbol{F}$ is the smoothing filter kernel illustrated in Figure 69, and $\boldsymbol{M}$ is a temporary map used to calculate the final smoothed T2/T2* value as:

$$\boldsymbol{T}_s = \boldsymbol{M} / (\boldsymbol{C} * \boldsymbol{F}) \tag{12}$$

where $\boldsymbol{T}_s$ is the smoothed T2/T2* value, $\boldsymbol{M}$ is the map calculated in Equation 11, / denotes pixel-wise division, $\boldsymbol{C}$ is the certainty map, $*$ denotes convolution, and $\boldsymbol{F}$ is the smoothing filter kernel.

44.13 Longaxis volumes

Volumes can be calculated using segmentation from longaxis images. The algorithm begins with automatically locating images labeled 2CH, 3CH and 4CH that contain segmentation. If the same kind of segmentation is found in two such images, the volume is calculated by rotating each segmentation area one full revolution around the axis of intersection and taking the mean of these volumes. If there are three images that contain the same segmentation, the volumes are calculated as described above for each pair of images, and the mean of these three values is used.

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